Pseudomon Antheraea Homo sapi Rattus no

Homo sapi

Ralstonia

Homo sapi

Xanthomon

AX256351 S AF026197 X M30933 · E.t AB045311 X AC090645 H AC646063 F AC055876 H AC084023 C

Mus muscu Mus muscu

AC090533

AF051726 Mus muscu AL603702 Mouse DNA

Mus muscu Caulobact Rattus no Rattus no Pseudomon Pseudomon

Homo sapi Drosophil

AC013433 AC098555

AE00457

score:

Title: Perfect sc Sequence:

nucleic

Run on:

Scoring table:

Searched:

Database :

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Hacter...

Xanthomonas.
Xanthomonas.
XS and XX., Fab.H. and Wei, Z.M.
Song XX., Fab.H. and Wei, Z.M.
Receptors for hypersensitive response elicitors and uses thereof
iAL Patent: WO 0170988-A8 27-SEP-2001;
Eden Bioscience Corporation (US)
Eden Bioscience Corporation (US)
Location/Qualifiers
ource
/organism="Xanthomonas campestris pv. pelargonii"
/db_xref="taxon:91612"
/ab. xref="taxon:91612"
/ab. xref="taxon:91612"
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Xanthomonas campestris pv. pelargonii
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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Sequence 8 from Patent WO0170988.
AX256351.1 GI:16075202
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                                                                            June 28, 2002, 10:21:53; Search time 1822.67 Seconds (without alignments) 3926.589 Million cell updates/sec
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                                                                                                                                                            342
1 atggactctatcggaaacaa......gcagcctgggcggcaacgcc 342
                                                                                                                                                                                                                                                                                 3595312
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                 1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters.
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Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Continuation (2 of AL355490 Human DNA AL646073 Ralstonia X80031 Homo sapien Continuation (12 o AF297658 Danio rer

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AC106604 AL646057 AC099436 AC099294 AE003589

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AB012767 AE001876 AF067607 AC099443 AL606742 AB073377 M15101 P.G

Mus musco

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PAT 10-OCT-2001

BASE COUNT ORIGIN

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Zhu,W. and White,F.F.
HprXo is a regulator of hrp gene expression in Xanthomonas oryzae
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2hu,W. and White,F.F.

Direct Submission

Submitted (12-SEP-1997) Plant Pathology, Kansas State University,
Throckmorton Hall, Manhattan, KS 66506, USA

4 (bases 1 to 10096)

White,F.F., Zhu,W. and Magbanua,M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-FEB-2000) Plant Pathology, Kansas State University, 4024 Throckmorton Hall, Manhattan, KS 66506, USA Sequence update by submitter
On Mar 30, 2000 this sequence version replaced gi:4003499.
Location/Qualifiers
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Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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/note="adjoins with sequence presented in GenBank

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 Length 342;
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    10096
/organism="Xanthomonas oryzae pv. oryzae"

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Zhu,W., MaGbanua,M.M. and White,F.F.
Identification of two novel hrp-associated
; DB 6;
1.5e-62;
nes 0;
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J. Bacteriol. 182 (7), 1844-1853 (2000)
            Pred. No. 1. 9
0; Mismatches
 Score 342;
Pred. No. 1
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/note="pathovar: oryzae"
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/translation="MIFRAAALACAAPFARADCFEEAAGYQHVNPWVLRAIAWQBSRGR
ADAIHRNNGTVDYGKWQINSIHLRRLFGYGISKEALMQPCVSVYVAAWRLREWTNKY
GNTWAAVGAYHSETPGERDKYAHAIHSILLRLGVMVNRASDPAGWRGAAMRMHRALHQ
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ASPSDRMPVSPPLPGSGAAAGSPASVWPELSKGRRDESNPIDAGGAELASDAPVIEA
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NKAKIVSSPQVATLDNVEAVMOHKQQAFVRVSGYASADLINLSAGVSLRVLPSVVPGS
PNGQMRLDVRIEDGQLGSNTVDGIPVITSSEIKTQAFVNEGQSLLIAGYAYDADETDL
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PGIARNGVIYVLSSFIAYGQPADALAKIQTVGLVGVVFKEAFIGLLIGFAASTVFWIA
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DGAMLRIWGANESKSATLSLGTASTKSLRDALARWRLDDSRFPVRYDEAAHVAVVSGP
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                                                                                                                                 protein; hrp-associated protein"
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Accession Number AF232058" complement(129, .908)
                                                                                                                                                                                                            /evidence=not_experimental
/product="Hpa2 precursor"
/protein_id="AAF61278.1"
/db_xref="G1:7350910"
                                                                                                                                 'note="lysozyme related
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/protein_id="AAC95122.2"
/db_xref="G1:7350909"
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/db_xref="G1:7350911"
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complement(4206. .5036)
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/note="HrcC related"
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/transl_table=11
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EIMMAX
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ESVGLLIDDLAGYNNVQMTNPLSGQOSTPVSTVLLQLAIVSFYALGGMLMLLGALFES
FRWPLTQLGPNMGAVAESFVIQQYDSMMAAVVKLSAPVMLVIVLVDLAIGLVARAAD
KLEPSNLSQPIRGVLALLLLALLISVFIAQFGEALGFLHFQQQLHDAANLGGKAGASH
                                                                                                                                                                                                                                                                                                         QDTEACTTRLADCDAALMDKTGVGGSINIDTILQHERFRTVLVEACRAAEQAQAAADQ
SLQSARDELASVQQALSKLQAQAQVYADKAASARRARQAQRDAAEEEDAIETLVALRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEPPTRRGFPPSVFAELPRILERAGMGESGSITAFYTYLAEDDTGSDPIAEEVRGILD
GHLILSREIAAKNQYPAIDVLASLSRVMSQIVPSDHSQAAGRIRRLLAKYNEVETLVQ
VGEYRQGSDAVADEAINRIDAIRDFISOPTDQLSDYESTLEQLANYTDDA"
                                                                                                                                                                                                                                                                                         /translation="MREPAYTWSVLHQLKARRCERMQERLSDCRRALEHCDRELARCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLAETPLLETTLERELATLAFGRRYGKVVEVVGTMLKVAGVQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEGORMGIFAAAGVGKSTLMGMFARGTQCDVNVIVLIGERGREVREFIELILGADGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSVVVCATSDRSSIERAKAAYVGTAIAEYFRDRGLRVLLMMDSLTRFARAQREIGLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSOAOARAOTLIEEAOOQAEAILHDAROKAERSARLGYAAGLRROLDEWNESGLRHAF
AAETAAHRARERLAEIVARTCEHVILGHDPAALYARAAQALEGALDEAKALRVSVHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mralrylvvllalllsacsqqlysglitendandmlevllhagvd
askvtpddgktwavnaphdqvsyslealrahglpherhanlgemfkkdglistpteer
VRFIYGVSQQLSQTLSNIDGVISADVEIVLPNNDPLATSVKPSSAAVFIKFRVGSDL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGEVCELRQRDGTLLQRAEVVGFSRDLALLAPFGELIGLSRETRVIGLGRPLAVPVGA
ALLGRVLDGLGEPSDGQGAIACDTWVPIQAQAPDPMRRLIEHPMPTGVRIVDGLMTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAPVYRRMRVIQAWSGWSELSPSALGVHANQLALIMPARLANVLIARALFSRGLAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCIERERLGWLEQCVGPAVLEHVRONASAGLSVPLLPRDADQAAWVGDGWRRMQADGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSNPVVAKLIALSLPLGAAQVATVAADGASAAFLTALPTLMPEASCVSG"
complement(8176..8937)
                                                                                                                                                                                                                                                /protein_id-"AAF61280.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAF61282.1"
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                                                                                                                                  complement(5033. .5542)
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                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5535, .6863)
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                                                                                                                                                                                                                                                                                                                                                                           complement(5535. .6863)
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                                                                                                                                                                                                                                                                    /db_xref-"GI:7350912
                                                                                                                                                                                                    /transl_table=11
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="HrpB5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRRVLAAPOEPADVG"
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/translation-"MTLIPPVQAIAGTSAAATQALSPVAAPNQALVNRFQALMQSSSP
LPPAMQRVGSPSMMSRVVDVQNDGVRTIAEHIDAFSMQAPTMGLQEMAAQQIKLMHEL
SLVPNIKTMVMHSVEGLTYENVSVTLVPGGAESDAQLTASAPPRPSPWPWVVGCVVTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="LRLLLKLLLLLLGQQKHWPERQQQQQPQPWLDRQQQQQHNQQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90348718
Draft entry and computer-readable sequence for [Unpublished (1990)
Synergen, INC., 1885 33rd St., Boulder, CO 80301] kindly submitted
by C.S.Ko 12-DEC-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1320 AGGGCAGGGGGGGGGGGGGGGGGGGGGATTCGCAGGCTGGGCAGC 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1380 AGAATGGCCCTCGCCATTCACCCAGATGCTGATGCTATCGTCGGAGAGATTCTCCAGG 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1440 CGCAGAATGGTGGTGGTGGTGGCGGGGTTCGGCGGCGGGTTCG 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ko.C., Smith,C.K.I.I. and McDonell,M.
Identification and characterization of a target antigen of a
monoclonal antibody directed against Eimeria tenella merozoites
Mol. Biochem. Parasitol. 41, 53-64 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 aggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcaga 280
                                                                                                                                                                                                                                                                                                                                                                                                                            161 agagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaac 220
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 accagggcggcgcggcatgggcggtggcggttcggtcaacagcagcctgggcgaacg
                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                     DB 1; Length 10096;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                        CLAGAAALYWWPNPOAGRWGGLQRLRELTTKGKAG"
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240 c 249 g 77 t
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E.tenella antigen LPMC61 mRNA, partial cds.
M30933
                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.tenella (strain Wisconsin), mRNA to cDNA.
Eimeria tenella
                                                                                                                                                                                                                                                                                                                                     Score 49.2; DB Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Eimeria tenella"
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/db_xref="G1:7350917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA29079.1"
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                                                                                              .9331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:5802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                     14.48;
54.48;
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DPRTNAILIRDRPERMOSYGTLIQQLDNRPKLLQIDATIIEIRDGAMQDLGVDMRFHS
QHTDIQTGDGRGGQLGFNGVLSGAATDGATTPVGGTLTAVLGDAGRYLMTRVSALETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRWWDLTQLGPNMGAVAESFVIQQYDSMMAAVVKLSAPVMLVLVLVDLAIGLVARAAD
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                                                                                                                                                                                                                                                                                                                                                  SIYGARGASVAPIAAFGANFGRVQPIGGGSSNTFGNAAQGQGGGASGTLGLPSAWFGG
ASPSDRMPVSPPLPGSGAAAGSPASVWPELSKGRRDESNPIDAGGGAELASDAPVIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNGOMRLDVRIEDGQLGSNTVDGIPVITSSEIKTQAFVNEGQSLLIAGYAYDADETDL.
NAVPGLSKIPLLGNLFKHRQKSGSRMQRLFLLTPHVVSP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESVGLLIDDLAGYNNVQMTNPLSGQQSTPVSTVLLQLAIVSFYALGGMLMLLGALFES
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SLQSARDELASVQQALSKLQAQAQVYADKAASARRARQAQRDAAEEEDAIETLVALRS
                                                                                                                                                                                                                                                                               YVADNKDLKEVLRDLSASQSIATWISPEVTGTLSGKFETSPQKFLDDLAATYGFVWYY
                                                                                                                                                                                                                                                                                                   DGAMLRIWGANESKSATLSLGTASTKSLRDALARMRLDDSRFPVRYDEAAHVAVVSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MREPAYTWSVLHQLKARRCERMQERLSDCRRALEHCDRELARCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lgevcelrordgilgtalgraevvgfsrdlallapfgeliglsretrviglgrplavpvga
allgryldgigepedggalacdtwvpiqaqapdpmrrliehpmptgvrivdglmtl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSVVVCATSDRSSIERAKAAYVGTAIAEYFRDRGLRVLLMMDSLTRFARAQREIGLAA
GEPPTRRGFPPSVFAELPRLLERAGMGESGSITAFYTVLAEDDTGSDPIAEEVRGILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLAETPLLETTLERELATLAFGRRYGKVVEVVGTMLKVAGVQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEGQRMGIFAAAGVGKSTLMGMFARGTQCDVNVIVLIGERGREVREFIELILGADGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGIARNGVIYVLSSFIAYGQPADALAKI
                                                                                                                                                               /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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/db_xref="G1:9711582"
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                                                                  complement(1384. .3201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3284. .4114)
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complement(5931. .6632)
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misc_feature
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complement(1384...3201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (28-JUN-2000) Hirokazu Ochiai, National Institute of Agrobiological Resources, Department of Genetic Resources I; 2-1-2 Agrobiological, Tsukuba, Ibaraki 305-8602, Japan (E.mail:cchiaih@abr.affrc.go.jp, Tel:81-298-38-7452, Fax:81-298-38-7408)
                                                                                                                                                                                                                                                                                                                      210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                    tcgccttcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatg 150
                                                                                                                                                                                                                                                                                                                                                                                                       211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
                                                                                                                                                      541 CAAGCGCAACAGTGGCAGGCGCAGCAGCAGCAGTGGCCGCAGCAGCAGCAGCAGCAGCCG 600
                                                                                        Gaps
                                                                                                                              Ochiai, H., Inoue, Y., Hasebe, A. and Kaku, H.
Construction and characterization of a Xanthomonas oryzae pv.
oryzae bacterial artificial chromosome library
FEMS Microbiol. Lett. 200 (1), 59-65 (2001)
                                                                                                                                                                                                                                                                                                            151 atgctgcaacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas oryzae pv. oryzae (strain:MAFF 311019) DNA.
Xanthomonas oryzae pv. oryzae
                                      Length 767;
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/strain="MAFF 311018"
                                                                                 0; Mismatches 129; Indels
                                        DB 3;
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Xanthomonas oryzae pv. oryzae DNA,
                                      Score 48.6;
Pred. No. 1.
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                                      14.28;
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                                                      Best Local Similarity
Matches 126; Conservative
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                                                                                               /translation="mrywlrstpdaigldcdvvprealasvlaldaaavevharceda
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                                                                                                                                                              ALDAARRAFDAAATKAGWTLQVELCGDADLAVGACVCEWDTGVFETDLRDQLRSLRRV
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                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDNTRIDNAARCVQRWTDALAQLAESLDAARVAHWLGPVAASGW
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9113. .10192
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9113. .17604
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16286)

2 (Loses 1 to 16286)

3 Luo,C., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F., Li,F., Li,T., Song,L., Song,Y., Sun,W., Sun,W., Sun,Y., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L., Wang,R., Wang,X., Wang,X., Wang,X., Yu,B., Zang,Y., Zhang,X., Zhu,B., Zhu,
                                                                                                                                                                                                                                                                                                                          /db_xref="G1:9711589"

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Homo sapiens chromosome 3 clone RP11-556G18 map 3p, complete
sequence.
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                                                                                                                                                          Wang, J., Wang, J., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wang, X., Wang, X., Wang, Y., Wang, X., Wang, X., Wang, Y., Wang, X., Wang, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 agagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaac 220
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Pred. No. 1.6;
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                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                /protein_id="BAB07858.1"
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/transl_table=11
                                                                                                                                                             /product-"Hrcu"
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Center code:Beijing
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Best Local Similarity
Matches 96; Conserv
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Blometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex Laboratoire de Genetique Cellulaire Christian Boucherfelulouse inra fr
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AMVRALAGKLNALRWTPELVGEFFGAYLTEPKDHVEFVTQPRLSLARFTARARKEGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MNELPLYAAARGVQPGLAAGRPAQLLGGLSPRDFMRTHWQKKPL"
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EEALDGHEQGFETKLQLEPDDAFGEYDQELIKIEPRDRFPEPLEVGMQFEGVPEDGDD
EDAIIYTVTDVAEDKVVLDGNHPLAGMALRFDLRVTDVREATAEEIEHGHVHGENGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="PROBABLE FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIRQALSPEDMRALHFPLSPDALIKLARREDVESRLIAQTRGRWTFNHG
                                                                                                                                                                                                                                                                                                                                                                                                  http://sequence.toulouse.inra.fr/R.solanacearum.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence-not_experimental
product = CONSENTED HYPOTHETICAL PROTEIN"
/protein_id="CAD14850.1"
/db_xref="GI:17428162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'function="cell processes; chaperoning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Product confidence : probable
Gene name confidence : probable
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ralstonia solanacearum"
/strain="GMI1000"
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/protein_id="CAD14851.1"
/db_xref="GI:17428163"
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1573. .2097
'qene-"slyD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(332. .1561)
/gene="RSc1148"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(332. .1561)
/gene="RSc1148"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                         Direct Submission
                                                              Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                   TITLE
JOURNAL
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        JOURNAL
                                REFERENCE
                                                           AUTHORS
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1 (bases 1 to 207050)
Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.
Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27433 CCAGTAGCAGCTCCAGCAGCAGCCCCAGCAGCAGCAGCAGCAGCCCCAGTAGCAGCT 27492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 ggatcagttgctcgccatgttcatcatgatgctgcaacagagccagggcagcgatgc 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 gacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-gcgggcggccggca 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum GMI1000 chromosome, complete sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 9; Length 162869;
Pred. No. 5.8;
0; Mismatches 140; Indels 1
                                                                                                                                                                                                                                                                                                                                                               Insert size: 162869; sum-of-contigs
Ouality coverage: 10.92x in 020 bases;sum-of-contigs
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                                                                                                                                            Sequencing wearth of the sequencing vector: pUC18: 100% of reads Chemistry: Dye-terminator: ET 58: of reads Chemistry: Dye-terminator Big Dye: 45% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 164941 bases at least Q40 Consensus quality: 165761 bases at least Q30 Consensus quality: 165761 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27553 GCCCCAGTAGCAGCTCTAGCAGCAGCAGCTCCAGCAGCAGC 27593
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                                                                      Center project Information
Center project name:1% project
Center clone name: RP11-556G18
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35618 c 35228 g 46181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .162869
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
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Website:http://hgc.igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                           http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
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Ralstonía solanacearum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="3p'
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AL646063
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FMLHVIAPLVADFRAQYPQIELELMTSDRIIDLLEEDTDVAIRIGALRDSTLRARRLG
TRRLRVLASPAYLKAHGRPRTVDALRHHALLGFVQPESLNHWPLRGPHGDRLRITPTL
KASSGETLRQLALQGAGIVCLADFWTARDRRAGDLVQVLPEATVEIQQPIHAVYYRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="G1:17428167"
/translation="MPIALLALFLSAFAIGTTEFVIVGLIPTVAADLGITLPSAGWLV
SLYALGVAVGAPVLTALTGRLPRKALLLALMALFTLGNLLAWRAPGYAPLVLARVMTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAVAGLGVIAFVGSLVFVPRDIAHAPPASLAROLQVLAQPRLLMVYAKTAIGYGGSFI
PFTFLAPILQDVAGFSAGAVGWYMLVYGVSVAAGNLWGGRLADRKGPIAALQVIFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAHGVFFSIGSTLATSLVPREKAASAIAIMFTCLTVALVTGVPLGTFIGQHFGWRETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAVLFAFTFTARYPWTAVATVLLWGAVAFGNVPGLQAYVVKQAERFAPQAVDVASGLN
IAAFNLGIAGAAWAGGWIVTHLGLMHTPWIGALVVLVSLGLTAWSGALDRRGGIGPRL
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                                                                                                                                                                                                                                    small molecules"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 cacgaggactccagccagcagtcgccttcggctggctccgagcagcagcagtggatcagttg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/product="PUTATIVE TRANSMEMBRANE EFFLUX TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatgggcggtggc 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53118 TGGGAAGCCGCCCGCCTGATGCGCGACGAGGACACCGCCGCCTATCTGCAGGTGCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 ctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 tgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 207050;
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Homo sapiens chromosome 15 clone RP11-578F21 map 15,
IN PROGRESS ***, 3 unordered pieces.
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                                                                                                                                                                                                                                 processes; transport
confidence : putative
                                                                                                                                                                                                                                                       /note="Product confidence : putativ
Gene name confidence : hypothetical
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0; Mismatches 177;
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                                                                                                                                                                                                                                                                                                          predicted by Codon usage predicted by Homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_1d="CAD14855.1"
                                                                     OLASRITCFLDVLEARLAGGE"
6966. .8168
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                                                                                                                                                                                                                                                                                                                                                                predicted by FrameD
                                                                                                   6966...8168
/gene="RSc1153"
/note="RS04598"
                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                    /function="cell
                                                                                                                                                                                                      /gene="RSc1153"
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/gene="RSc1154"
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AC055876.5 GI:17386491
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                                                                                                                                                                                 . .8168
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Best Local Simi
Matches 150;
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AC055876/c
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LFHIRARRLASDIAPSTPQQ"
                                                                                                                                                                                                                                                                                                    /translation-"MARPGAAFRAWRGIAAALAMLAATAAPAAPKGHATAAPAAPACF
                                                                                                                                                                                                                                                                                                                               TFAVVGNVPQRPEDVAPARALLDAIDTEHPAFVVHI.GNLKGRDESCTDNLLEERHDLL
                                                                                                                                                                                                                                                                                                                                                     DSTITPLIYIPGDHDWSDCGRPTAGRFDPIERLLRLRDLFYPDDNALGORTWTVMRQS
                                                                                                                                                                                                                                                                                                                                                                                DQAKFRSYRENARWETGGVLFVTLNVPGDNNNYKTAGGRNGEYEDRLEANRQWLARAF
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GDFYELFFEDAEKAARLLDITLTSRGTTNGQPIRMAGVPFHAVEQYLAKLVKLGESVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVEAGARRLREQLGVASLVAFGCETLTAALAAAGALLNYAAATQGQSLRHVIGLTVEH
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PQARQQAIEVLLAGDWQSLRGTLRTLSDVERITGRLALLSARPRDLSSLRDTLARLPE
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QADVLATLAERAHALSWSRPALTDAPG IELIRARHPVVEQQVEQFYANDCVLQETRKL
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PVIRAARKRLAWLEQHSADTGATPQLDLFALPSDPSDDDAAEAAAPAAPSALAEALDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICEQIGDPATTKGPVERKVVRVVTPGTLTDAALLSDKVNNHLLAIAQIPGKRGAAPLV
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LETTLLSRTTRRLALTDEGTAFLAHARGILAAVDEAEELIALRRQQPAGRLRVNAAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesis, modification; dna - replication, repair, restr./modif...
/note="Product confidence: probable Gene name confidence: probable predicted by Codon usage predicted by Homology predicted by FrameD*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="miscellaneous; not classified.regulator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="macromolecule metabolism; macromolecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="PROBABLE DNA MISMATCH REPAIR PROTEIN"
/protein_id="CAD14853.1"
                                                                                                                                                                                                 /evidence=not_experimental
/product="PROBABLE TRANSMEMBRANE PROTEIN"
/protein_id="CaD14852.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable
                                             /note="Product confidence : probabl
                /function="miscellaneous; unknown"
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Gene name confidence : hypothetical
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                                                                                                predicted by Codon_usage predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="RSc1151; RS04600"
complement(3216. .5864)
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predicted by Homology
predicted by FrameD"
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/db_xref="G1:17428166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3216. .5864)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5960. .6853)
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                                                                                                                                                                           /transl_table=11
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                                                                                                                                                   /codon_start=1
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/transl_table=
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Anderson 1. (Juston, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barraa, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barraa, N., Bastien, V., Beda, F., Bagouslano, A., Castle, A., Chepepl, Y., Colangelo, M., Collins, S., Campoplano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Galagan, J., Gardyna, S., Glode, S., Gyottle, M., Graham, L., Gade, D., Grand, P., Bartellano, K., Marford, M., Graham, L., Carant, G., Hagos, B., Haaford, A., Horton, L., Kalin, J., Lamoscque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., Mirowa, T., Minda, C., Mengay, V., Morrany, K., Meldrin, J., Menenus, L., Mhova, T., Miranda, C., Mengay, V., Morrany, C., Norman, C., Pollara, V., Raymond, C., Riley, R., Peterson, K., Peterson, K., Petenson, K., Peterson, K., Petenson, K., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J., Vous, S., Santos, R., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J., Vous, S., Santos, R., Stange-Thomann, V., Limer, A., Milson, B., Wu, X., Wyman, D., Ye, W., Subnission, M., Subramanian, A., Trigilio, J., Vous, C., Markett, M., M
                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/clone_lib="RPCI-11 Human Male BAC"
38922 c 39919 g 57756 t 329 others
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                  1 (bases 1 to 190770)
Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 15, clone RP11-578F21
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/chromosome="15"
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AC084023 178984 bp DNA linear HTG 05-FEB-2002 Oryza sativa chromosome 10 clone OSJNBa0062C05, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.
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1 (bases 1 to 178984)

Buell, R., Hsiao, J., Zismann, V., Moffat, K.M., Hill, J., Gansberger, K., Burgess, S., Jarrahi, B., Shvartsbeyn, M., Brenner, M., Feldblyum, T., Khalak, H.G., Yuan, Q., Quackenbush, J., White, O., Salzberg, S. and Fraser, C., Quackenbush, J., White, O.,
                                                                                                    Db 183403 GAAGCAGGAGCAGATGCGGAAGCAGGAGGAGAAGCAGAAGCAGGAGGAGGAGCAGAT 183344
                                                                                                                                                                           Submitted (10-CCT-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
On Feb 5, 2002 this sequence version replaced 91:18464087.
                                                                                                                                                171 cagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcct 230
                                                                gcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccaggg 170
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* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 17994: contig of 17994 bp in length
                                 0; Gaps
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gap of unknown length
contig of 85415 bp in length.
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of 57011 bp in length
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51720 a 37144 c 39186 g 50461 t
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/db_xref="taxon:4530"
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2 (bases 1 to 178984)
Best Local Similarity 52.8%;
Matches 93; Conservative
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Homo saplens chromosome 5 clone RP11-404K5, *** SEQUENCING IN
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 60 Aug 28, 2001 this sequence version replaced gill433887.

* NOTE: This is a working draft' sequence. It currently consists of 4 contigs. The true order of the pieces:

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will
                                                                                                                                                                               Db 124695 Grecrcaagaagergaageagaagercaagaagarcaagaacarcaccecegeegee 124754
                                                                                                Db 124635 GCGGAGGAGGAGGGGGACAGGGGCAGATGCACCGTGGGGAGGAGAAGCACAAGCCG 124694
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                                                              gcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggectgagtccg 237
                                                                                                                                             Quality coverage: 1 in Q20 bases; sum-of-contigs
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Catarrhini; Hominidae; Homo.
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                         Indels
                                                                                                                                                                                                                                                            Db 124755 GGCGGCGCCACGCCGGAACAACGCGCGGGGGCGCGCGTAGCG 124797
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      Pred. No. 15;
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Mammalla; Eutheria; Primates;
1 (bases 1 to 159971)
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Matches 88; Conservative
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AUTHORS
TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrouk, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, W.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93102 AGCAGATGCGGAAGCAGGAGCAGATGCGGAAGCAGGAGGAGCAGCAGTAGCGGAAGCAGG 93161
                                                                                                                                                                                                                                                                                                                                                                                                                          92982 CGGGGGAGCAGGAGGAGCAGATGCGGAAGCAGGAGGAGCAGATGCTGAAGCAGAAGAGC 93041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93042 AGATGGGGAAGCAGGAGGAGCAGATGGGGGGAGCAGGAGGAGCAGATGCGGAAGCAGAGGAGG 93101
                                                                                                                                                                                                                                                                                                                                                                     107 ccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagcc 166
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on 27 of 529 of the complete
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                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 agggcagcgatgcaaatcaggagtgtggcaacgaacaacagaacggtcaacaggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 gcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg
                                                                                                                                                                                                                                                        Length 159971;
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                                                                                                                                                                                                                                                     Score 42.4; DB 2;
Pred. No. 21;
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/rransl_table=11
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                                                                                                             /clone="RP11-404K5"
a 32108 c 33093 g 47871 t
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Pseudomonas aeruginosa PA01, section
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                          /db_xref="taxon:9606"
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Nature 406 (6799), 959-964 (2000)
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1. .159971
/organism-"Homo
                                                                                     /chromosome="5"
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Best Local Similarity
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LAKKEQGGENFEIVVPSISILAEPPVAVVDKVVEKKGTRKVAEATLQYLYSEEGGRIA
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LRHKDGDYRWIHSRGRVLRDALGKPLHYTGVARDITLQRLKEDHLRQAAAVFDSTREG
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WSGEIWNRRKSGEIYPQWLHIRAVRNDQGQLTHYVGFFSDLSSIKRSENELDFLAHHD
SLTGLPNRVLLRERIEQALENGKDRTVAGALLLIDLDHFKHINDSLGHTTGDMLKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALDNWYLKRACROMREWOORGYELFVAVNYSSRLFNRGGLEERIANALEESGLEPRY
LELEVTESAVMEDFEGSLNLLCRLRILGVNLAIDDFGTGYSSLMRLKRLPVHKLKIDO
GFVAGLPGAVDDAAIARAIVALAQSMGLRVVAEGIEHODQALFLREHGCDFGGGYWYG
                                                                                                                                                                                                                         DWQARLPDNSTPYTST1VFLVRKGNPKG1KDWGDLTKEGVEV1TPNPKTSGGARWNFL
                                                                                                                                                                                                                                                           AAWAWAKKQYGSDEKAKDYVQALYKHVPVLDTGARGSTITFVNNQ1GDVLLAWENEAF
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SASLGVSLYPEDASDVDHLMQHADAALFQAKDSGRNAYAFYTRVLTARARAHVQVESA
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HPALQHFFRFWLWLTTGMNTREWTAIHRKHHAKCETVEDPHSPVHKGLFTVLRAGAEL
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SYKKWEEDLOMANIKLESFLRLARVARVARPIAHRYBGKHSLDMTYAMALINNROJIM
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KVIYEKRLALQOIWAKTSANGHDMLAAIKDWVHEABASGIQSLKEFAAQLKTYSERRA
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/gene="PA0286"
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ALGIORDELVAALGESSASTLALAVTLGVTGVGLATGALTAVTGVFVIPAVPYLG
ALGIORDELVACALGESSASTLALAVTLGVGLAGDLEPQMLGASLLTLVPALGGMLLGO
WLRORISATLFRRCFFVGLLLLGADLAWRGFH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-MOFNPGFSSLAALLADPGRAQMIWALMDGSARPASELALLAGVS
SSASGHLGERUVEGGYLSLEARGRNRFXLAGPECQAVEALASASLADPGPRSLPP
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DEPFGALDAKVRKELRRWIARLHEEINLTSVFVTHDQEBAMEVADRIVVMNKGVIEQI
GSPGEVYENPASDFVYHFLGDSNRLQLGNDQHLLFRPHEVSLSRSAVAEHRAAEVRDI
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VPFYARELIPLMQEGGTQEEEAARLLGANGMOMFWHVTLPNIKWGLIYGVVLCTARAM
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VLADIPKEVEBAAACLGARPLQVFRHILVPALLPAWLTGFALAFARGVGEYGSVIFIA
GNMPMKTEILPLLIMVKLDQYDYTGATAIGVLMLVVSFILLLLINLLQRRIETP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MSIEIRNVSKNFNAFKALDDINLDIQSGELVALLGPSGCGKTTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSRRISPVIPGFGLTLGYTLVYLSLLVLIPLGAMFLKTTQLSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFWAIISAPRVLAALKLSFGTALAAAVLNGLIGTLILAWVLVRYEFPGRKIIDAMIDLP
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                                                                                                                                                                                                                                                                                                                                                              /transi_table=11
/product="probable_transcriptional_regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="sulfate transport protein CysA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="sulfate transport protein Cysw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein CysT"
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/db_xref="GI:9946125"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAG03669.1"
/db_xref="G1:9946123"
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/db_xref="G1:9946124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1674. .2663)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1674. .2663)
/gene="cysA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2667. .3536)
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/note="PA0282"
complement(3547. .4365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3547. .4365)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4527. .5525)
/gene="sbp"
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/transl_table=11
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                                                                                                                                                                                                                                  /gene="PA0279"
963. .1661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="cysA"
/note="PA0280"
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/note="PA0281"
                                                                                                                                                                                                                                                                                                      /gene="PA0279"
                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start-1
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AAARVLLPDLAVPENAYAEITREVLAPGLRGIVVAAALSAIMSTASGCILAAARVLQE
DIYARFLRPGTTSDIRLSRCITLLMGVAMLVLACIVNDVIAALSIAYNLLVGGLLVPI
IVYSVIGGMWSLTLTDIIQFVIKTVGIFLVLLPLSIDGAGGLARMQEVLPAGFFDLGH
                                                                                                                                                         VGALLWRRASPQGAIASIVAGCLAVIACMARDGLLANSPIVYGLLASLATFVAVSLAT
RPAASLRAQPE
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Kim,Y.-S., Lee,K.-S., Goo,T.-W., Yun,E.-Y. and Kim,K.Y..
Complete nucleotide sequence of fibroin gene cloned from Antheraea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-DEC-2000) Department of Sericulture and Entomology,
National Institute Agriculture Science and Technology, RDA 61
Seodun-dong, Kwonseon-gu, Suwon 441-100, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3446 crédrorredeceretrecres de la constant de la co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagtigcicgccatgitcatcatgaigaigcigcaacagagccaggggagcgaigcaaai 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatgggc 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 108; Indels . 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Bombycoidea; Saturniidae; Saturniini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caggagtgtggcaacgaaccacgcagaacggtcaacaggaaggcctgagtccgttgacg
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Kim,Y.-S., Lee,K.-S., Goo,T.-W., Yun,E.-Y. and Kim,K.Y.
Direct Submission
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/organism="Antheraea yamamai"
/db_xref="taxon:7121"
/transposon="mariner-like element"
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                                                                                                                                                                                                                                                                                                                                                                                                        tch 12.3%; Score 42.2; DB 1; al Similarity 49.8%; Pred. No. 27; 107; Conservative 0; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="nonfunctional transposase
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/product="fibroin"
join(1672, .1713,1864. .9789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3266 GCCTGGTGCGTGAGCAAGTTCGAGTTTCGCGGCAA 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggtggcggttcggtcaacagcagcctgggcggcaa 338
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                                                                                                                                                                                                                                      11352. .12308
/gene="speB1"
/note="PA0288"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF325500.1 GI:15077405
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AUTHORS
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AF325500
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/translation-"MRVTafVILCCALQYATANNLHHHDEYVDNHGQLVERFTTRKHY
ERNAATRPHLSGNERLVFTIVLEEDPYGHEDIYEEDVVINRVPGASSSAAAASSASAG
                                                                                                                                                                                                                                               GSGRGYGWGDGGYGSDSAAAAAAAAAAAAAGSGAGGAGGDYGWGDGGYGSDSAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAARRAGHDHAAGSSGGGYSWDYSSYGSESAAAAAAAAAAGSGAGGVGGGYGGGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccag--ggcggcggccggc 297
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Pred. No. 31;
0; Mismatches 125; Indels
                 /protein_id="AAK83145.1"
/db_xref="G1:15077406"
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/product="fibroin"
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9851. .9856
a 2274 с
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Best Local Similarity 50.4%;
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavki, L., Boukhgalter, B., Baddwin, J., Sastle, A., Castle, A., Calines, S., Collymore, A., Castle, A., Castle, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewark, K., Domino, M., Donelan, L., Doyle, M., Firzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 11, 2002 this sequence version replaced gi:14209777.

All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                  bp DNA linear HTG 11-FEB-2
*** SEQUENCING IN PROGRESS ***, 5
2749 GCCGCAGCTGCAGCAGCAGCAGCTTCAGGTGCTGGAGGATCAGGCGGCGGTTACGGA 2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome/Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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103898 126333; contig of 22436 bp in length
126334 126433; gap of 100 bp
126434 142277: contig of 15844 bp in length.
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24513 46948: contig of 22436 bp in length
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47049 103797: contig of 56749 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 142277)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-25C1
                                                                                                                                                                                                                                                                                    Homo sapiens clone RP11-25C1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Oualifiers
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                                                                       unordered pieces.
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TITLE
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AUTHORS
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COMMENT

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"S Muzny, Dh. Addractuda, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Charle, J.C., Cher, G., Chen, R., Coyle, M.D., Dathorne, S.R., David, R., David, C., Claveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gall, K.J., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gall, R., Ganer, T., Garza, N., Gall, R., Gao, J., Garcia, A., Hale, S., Hamilton, K., Harris, K., Johnson, R., Joluet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Lidharqe, O., Lieu, C., Liu, J., Liu, M., Lux, Lucier, A., Lucier, R., Luna, R., Marlindale, A., Marlindale, A., Marlindale, R., Mawhiney, E., Michel, M., Merier, R., Markin, P., Marlindale, R., Harris, R., Markin, R., Martindale, R., Harris, R., Markier, R., Martindale, R., Harris, R., Markier, R., Harris, R., Markier, R., Martindale, R., Markier, R., Martindale, R., Markier, R., Mar
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Rattus norvegicus clone CH230-108D18, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 132092 GCTGAAGCAGAAGGAGCAGACGGAGCAGGAGGAGCAGNNNNNNNACGGGGGAGCAGGA 132151
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 aaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgtt 239
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                                                                                                                                                                                                                                          566 others
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                                                                                                                                          /clone="RP11-25C1"
/clone_lib="RPCI-11 Human Male BAC"
39176 a 32698 c 33584 g 36253 t 566 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2;
Pred. No. 25;
1. .142277
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Rattus norvegicus
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Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, R., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Yunson, R., Watlington, S., Warley, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Williams, G., Williamson, A., Strilla, S., Nelson, D., Direct Subalssion
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NOTE: This is a "working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                       Submitted (12.JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 148335 bases at least 040 Consensus quality: 155812 bases at least 030 Consensus quality: 162105 bases at least 020 Estimated insert size: 157288; sum-of-contigs estimation quality coverage: 0x in 020 bases; agarose-fp estimation quality coverage: 2.4x in 020 bases; sum-of-contigs estimation
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is not known and their order in this sequence record

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Jia, H., Zhang, P., Lih, S. and Roe, B.A. Mus musculus BAC Clone rp23-422n18
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Direct Submission
Submitted (28-JUN-2001) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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On Jan 29, 2002 this sequence version replaced gi:18139426.
On Jan 29, Editor this sequence version replaced gi:18139426.
Center: Department of Chemistry And Biochemistry
The University of Oklahoma
Center code:UOKNOR
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HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
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NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 272545)
Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M.,
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Pred. No. 36;
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/organism="Mus musculus"
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/note="assembly_name:Contig108"
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/note="assembly_name:Contig107
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                                                                        Li,L., Montgomery,K.T., Grills,G., Chlu,D., Decker,J., Fusina,M.,
Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,
Perera,A., Shim,C., Thomas,E. and Rucherlapati,R.
Direct Submission
                                                                                                                             Submitted (02-MAR-2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave. Bronx, NY 10461, USA On Dec 21, 2001 this sequence version replaced gi:13310871.

Center: Harvard Partners Genome Center Center Code: HPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: agarose-FP - N/A Quality coverage: 6.8 x in Q20 bases; sum-of-contigs estimation
Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,
Perera,A., Shim,C., Thomas,E. and Kucherlapati,R.
High Throughput Mouse Sequencing
Onpublished
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in unknown length
g of 30444 bp in length
if unknown length
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Themistry: Dye-terminator Big Dye; 1008

Consensus quality: 257441 at least Q20

Consensus quality: 253718 at least Q30

Consensus quality: 247095 at least Q40
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                            TITLE
JOURNAL
REFERENCE
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JOURNAL
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us-09-829-124-1.rge

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Score 40.8; DB 2; Length 272545; Pred. No. 43; 0; Mismatches 127; Indels 0; Gaps Query Match 11.9%; Best Local Similarity 48.0%; Matches 117; Conservative

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102 tggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaaca 161 á

Db 178403 GCAGCAGGAGCAGCAGCAGGAGCAGCAGCAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCA 178344

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222 ggaaggeetgagteegttgaegeagatgetgatgeagategtgatgeagetgatgeaget ç

282 ccag 285 ŏ

Db 178223 GCAG 178220

Search completed: June 28, 2002, 11:23:05 Job time: 3672 sec

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June 28, 2002, 10:22:48 ; Search time 177.26 Seconds (without alignments) 3312.562 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                          1736436 seqs, 858457221 residues
                                                                                     OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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/SIDSI/goddata/geneseq/geneseqn-embl/NA1991.DAT./SIDSI/goddata/geneseq/geneseqn-embl/NA1991.DAT./SIDSI/goddata/geneseq/geneseqn-embl/NA1993.DAT./SIDSI/goddata/geneseq/geneseqn-embl/NA1994.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1995.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1995.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1995.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./SIDSI/goddata/geneseqy/geneseqn-embl/NA1998.DAT./ /SIDSI/gcgdata/geneseq/geneseqn-embl/NAzuou.bar:-/SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001a.bar:-/SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001B.bar:/SIDSI/gcgdata/geneseq/geneseqn-embl/NA2002.bar:-/SIDSI/gcgdata/geneseq/geneseqn-embl/NA2002.bar:-

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Xanthomonae campae	Nephila clavines s	Enstein Barr Virus	Drosophila melanog	Human NA Andria	D Dutida KT3440-a	DNA encoding nowel	DNA seguence of bu	Hypersensitive res	
		ID	AAD18127	AAT85356	AAX90924	ABL23322	AAA51260	AAF61055	AAS79854	AAC84677	AAT49316	
		DB	22	18	20	23	21	22	23	22	18	
		Match Length DB ID	342	2004	1925	3840	3121	1581	4335	5120	1035	
ф	Query	Match	100.0	11.3	11.2	11.2	11.1	11.1	11.1	11.1	11.0	
		Score	342	38.8	38.4	38.4	38	37.8	37.8	37.8	37.6	
	Result	So.	1	7	m	ი 4	2	U	c 7	&	σ	

23-MAR-2000; 2000US-191649P.

	Pseudomonas solana	ě	DNA encoding a hyp	Pseudomonas solana	DNA encoding a hyp	Pseudomonas solana	Drosophila melanog	Drosophila melanog		Drosophila melanod	Human secreted exp	Human reproductive	N.clavipes draglin	Nephila clavipes s	N. clavipes spider	MiSP1-containing p	Drosophila melanod	Human reproductive	Pseudomonas aerugi	DNA encoding angio	Human reproductive	Protein requiating	Drosophila melanog	Human immune/haema	Human immune/haema	Human secreted pro	Human cDNA clone (Human polynucleoti	Human cDNA sequenc		Mycobacterium tube	Human polynucleoti	Xanthomonas hrf1 p	Nucleotide sequenc	E. tenella cGMP de
AAV54609	AAV399/5	AAV 304 30	AAV63991	AAD006/4	AAA14944	AAD12808	ABL23323	ABL05117	ABL05116	ABL27665	AAA42475	AAL01496	AAQ14183	AAV23249	AAZ38195	AAQ98470	ABL27664	AAL05260	AAS51554	AAZ45239	AAL01459	AAZ57853	ABL09166	AAK72397	AAK72395	AAC02116	AAH05110	AA161196	AAH17588	AAI59410	AA199683	AAI81388	AA164895	AAV29159	AAC64577
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37.6	37.6	27.6	37.0		37.6	37.6	37.4	37.4	37.4	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37	37	36.8	36.6	36.6	36.6	36.6	36.4	36.4	36.4	36.4	36.4		36.2	36.2	m	35.8
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ALIGNMENTS

AAD18127 standard; cDNA; 342 BP.

RESULT AAD181

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Plant pathogen; hypersensitive response elicitor; HRE; stress resistance; disease resistance; Erwinia amylovora hypersensitive response elicitor; harpin; signal transduction; growth enhancement; insect control; virucide; fungicide; antibacterial; ss. /product= "Xanthomonas campestris hypersensitive response elicitor protein"
/note= "CDS does not include stop codon" Xanthomonas campestris hypersensitive response elicitor protein cDNA Location/Qualifiers 19-MAR-2001; 2001WO-US08728. (first entry) 1..342 /*tag= a /partial Xanthomonas campestris. WO200170988-A2 18-DEC-2001 27-SEP-2001. AAD18127; Key AAT85356 standard; DNA; 2004 BP.

us-09-829-124-1.rng

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The present invention relates to an isolated protein which serves as a receptor in plants for plant pathogen hypersensitive response elicitors (HRE). The plants are made resistant to infection by viruses, bacteria and fungl and are imparted with resistance against environmental stress and fungl and are imparted with resistance against environmental stress and insects through HRE treatment. The protein is useful for understanding the harpin (Erwinia amylovora hypersensitive response elicitor) induced signal transduction pathway in plants. The protein is useful for studying the downstream components of signal transduction pathway in plants which eventually leads to disease resistance, growth enhancement, insect control and stress resistance. Imparting disease resistance to plants through HRE treatment has the potential to treat previously untreatable diseases, treating diseases systemically which might not be treated separately due to cost and avoids the use of infectious agents or environmentally harmful materials. By HRE treatment enhanced plant growth is achieved which includes greater yield, increased quantity of seeds produced, increased percentage of seeds germinated, increased plant size, greater biomass, more and bigger fruits, etc. which results in economic benefit to cultivators. Greater yield, increased size and enhanced biomass allow greater revenue generation from the given plot of plant. The present sequence is protein chan.
                                                                                                                                                                                                                     New plant pathogen hypersensitive response elicitor-receptor protein isolated from plants, which upon silencing is used to study plant signal transduction pathways leading to disease resistance and growth
                                                                                                                                                                                                                                                                                                                                                    Oisclosure; Page 19; 78pp; English.
                                              (EDEN-) EDEN BIOSCIENCE CORP.
01-DEC-2000; 2000US-250710P.
                                                                                                Fan H, Wei
                                                                                                                                         WPI; 2001-590177/66.
                                                                                                                                                                         P-PSDB; AAE10807
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                                                                                             Song X,
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Sequence 342 BP; 83 A; 94 C; 109 G; 56 T; 0 other;

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                                                                                                                           121 gatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagggtgg 180
                                                                                                                                                                                                                  121 gatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgca 180
                                                                                                                                                                                                                                                                    acgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatg 300
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                                                                1 atggactctatcggaaacaacttttcgaatatcggcaacctgcagaggatgggcatcggg 60
                                 0; Gaps
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 100.0%; Score 342; DB 22; Length 342; 100.0%; Pred. No. 3.8e-79; ive 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.

Matches 342; Conservative
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RESULT AAT85356

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encoding silk protein. The process involves: (a) selecting target DNA, crown a silk-producing spider, that contains many repetitive and non-repetitive regions; (b) selecting a single-stranded DNA primer of at least 10 nucleotides with a sequence that is complementary to a region of the target; (c) repetitively combining the primer with melted target. DNA, incubating the mixture with nucleotides and a DNA polymerase with profereding activity to produce a DNA fragment which is complementary to the target and is at least 2 kb long. The present sequence represents a 2 kb DNA sequence which encodes the spider silk protein from Nephila clavipes. The DNA fragment can be used to make fibres, films, woven articles, e.g. for use in parachutes, sails, body armour, and absorbers (e.g. of heavy metals, biological weapons, DNA, chemicals, flavours and fragrances). The high molecular weight (90-250 kD) of spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins).
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                                                                                                                                                                                              High strength film; fibre; woven article; parachutes; sails; absorber; body armour; heavy metal; biological weapon; chemical; flavour; fragrance; Nephila clavipes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contg. both repetitive and non-repetitive sequences, useful for making high strength films, fibres, woven articles etc.
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                                                                                                                                                  Nephila clavipes spider silk protein 2 Kb DNA sequence.
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                                                 AAT85356;
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Antigen 1 (EBNA 1), which is obtained from commercially available plasmid pcWYEBNA. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orig) and agene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant cell lines expressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes. In transfected cells. The episomes are useful in the transfection of genes encoding receptors, transporter proteins, ion channels, adhesion
                                                                                                                                                                                                                                                                                                                                                      episome; transfection; origin of replication; EBV orip; receptor; everaporic host cell; recombinant cell line; ion channel; gene therapy;
873 acaaggtggctatggaggacttggaagccaaggtgccggacgaggaggattaggtggaca 932
                                     289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a 5
                                                                                                                                                                                                                                                                                                                                                                             multiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
                                                                                                                                                                                                                                                                                                                                    Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV orip; receptor;
                           230 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcg
                                                           933 aggtgcaggtgcagcagcagcagcagcagctggaggtgccggacaaggaggactaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             long, but
in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for expressing genes from recombinant eukaryotic cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virus Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except= (pos:799..800, aa:Gly)
/note= "The sequence is described throughout the specification as being 1926 nucleotides long, but sequence of only 1925 bp has been given in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a DNA encoding Epstein Barr
                                                                                                                                                                                                                                                                                                  Virus Nuclear Antigen 1 (EBNA 1) DNA.
                                                                                                                                                                                                                                                                                                                                   Antigen 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robbins AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "EBNA 1"
                                                                                                                                                                                                    AAX90924 standard; DNA; 1925 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Fig 2; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US03307
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                                                                                                                                                                                                                                                                                                                               Epstein Barr Virus Nuclear
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                           993 acaaggtgctggac 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PHAR-) PHARMACOPEIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                              cell immortalisation; ds
                                                                                          290 gcgccggcatgggc 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-610610/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Epstein-barr virus.
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                                                                                                                                                                                                                                                                                                Epstein Barr
                                                                                                                                                                                                                                                                   17-JAN-2000
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06-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                102 tggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaaca 161
                                                                                                                                                                                                                                                                                                                    ggaaggectgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaa 281
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                    676 дудусаудадусаддадсаддадудадудсаддадсаддаддадсаддадсаддаддад
                                                                                                                                                                                                                                                      gagocagogotatgoaaatcaggagtgtggoaacgaacaaccgcagaacggtcaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 21439;
                                                               Length 1925;
                                                                                                                                                                                                                                                                                                                                                                               282 ccagggcggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcggca
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                                                                                             Indels
           Sequence 1925 BP; 486 A; 352 C; 872 G; 215 T; 0 other;
                                                                            Pred. No. 2;
; Mismatches 161;
                                                               DB 20;
                                                          Score 38.4;
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                                                           Query Match
Best Local Similarity 45.6%;
Matches 135; Conservative
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
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                                                                                                                         42
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(ABB57737-ABB72072)

molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.

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WPI; 2000-431586/37.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                   2843 TCGATGGCATCAGCGATGCTGGCGACTCTGGAGCTGGACTACTTCAGGGCGGTGTCCCTC 2784
                                                                                                                                                                                                             2723 CACGATGGCCATGTCCAACTGTTCACCACCAAGGAGGAGGAGGAGGAGGAGCAGCAG 2664
                                                                                                                                                                      tcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctg 156
                                                                                                                                                         caacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggt 216
                                                                                                                                                                                                  caacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatg 276
                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product- PRO539
/note= "A putative Drosophila Costal-2 homologue"
                                                                                                                                                                                                                                                                                                                                                                                              PRO539; Costal-2; homologue; kinesin-related; Hedgehog; signalin
secreted protein; transmembrane protein; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W, Goddard
Watanabe CK;
                                                                      Score 38.4; DB 23; Length 3840;
Pred. No. 2.4;
0; Mismatches 121; Indels 0;
                                                                                                                                                                                                                                                      277 cagaaccagggcggcgggcatgggcggtggcggttcggtcaacagcagcc 328
                                        Sequence 3840 BP; 954 A; 915 C; 880 G; 1091 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fong S, Gao
A, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                            Human DNA encoding PRO539, a Costal-2 homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrara N, Fo
, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
186..2678
/*tag= a
                                                                                                                                                                                                                                                                                                               AAA51260 standard; cDNA; 3121
                                                                     Ouery Match 11.2%;
Best Local Similarity 47.8%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0119537.
99US-0119965.
99WO-US12252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0119341
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99US-0115565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200036102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     26-SEP-2000
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Gurney AL, I
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1999;
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16-DEC-1998;
22-DEC-1998;
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02-JUN-1999;
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12-JAN-1999
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10-FEB-1999
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                                                                                                                                                                               Costal-2 is a kinesin-related protein in the Hedgehog signaling pathway. The invention concerns novel secreted and transmembrane proteins, designated PRO polypeptides. The cDNA and gene sequences are useful in the recombinant production of PRO polypeptides, as a hybridization probe to screen libraries to isolate cDNAs with sequence identity to PRO polypeptides or to map the gene encoding the PRO polypeptides and analyzing genetic disorders. The cDNA/gene can also be used to produce transgenic animals useful for the development and screening of therapeutically useful reagents. They can also be used the gene therapy, e.g. to replace a defective gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1980 gaggagcagcaccagcagcagattgccttctcggaactggagtgcagctggaggagcag 2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2040 cagaggetggtgtactggetggaggtggeettggagegegegegeetggagatggacege 2099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 gagcagcagctggatcagttgctcgccatgttcatcatgatgatgcagcaacagagccag 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggc 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                           nucleic acid mólecule encodes a PRO polypeptide which is
                                                                                                                                                         This cDNA encodes PRO539 a putative Drosophila Costal-2 homologue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 3121;
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Pred. No. 2.9;
0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3121 BP; 702 A; 820 C; 1114 G; 485 T; 0 other;
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DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
MEDIZINISCHE HOCHSCHULE HANNOVER.
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                                                                                                              Claim 1; Fig 3; 154pp; English.
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                                                              transmembrane polypeptide
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Best Local Similarity 48.2
Matches 107; Conservative
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P-PSDB; AAY96730
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(GBFB )
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ful as other

useful

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This invention describes novel DNA sequences (I) for specific detection of Seademonas putida KT2440. The invention also describes (1) coff Seademonas putida KT2440. The invention also describes (1) cutaryotic cells transformed or transfected with (I) or the vector of (1); (3) production of expression products by culturing cells of (2); (4) expression products, or their fragments, of (1) and synthetic corrections or peptides with the same sequences (A); (5) poly- or proteins or peptides with the same sequences (A); (5) poly- or considerable and inibodies (Ab) that react specifically with (A); (6) plants that contain transformed or transfected cells of (2); (7) transgenic plants that contain transformed or transfected cells of (2); (8) considerable or more (I). (I), and their fragments, are used so probes to detecting KT2440 using a labeled (I) or Ab as probe; and (9) DNA chips carrying one or more (I). (I), and their fragments, are used for detecting the presence of KT2440, particularly in presence of other, or antibodies that recognize their expression products, are used for detecting the presence of KT2440 particularly in presence of other, or antibodies that recognize their expression products, are used for detecting the presence of KT2440 particularly in presence of other, or an as safe, by the National Institutes of Health, for genetic engineering work, e.g. as microbial production strains, for biological remediation and as vaccine carriers (I) are exclusive to KT2440 with no significant homelogy with sequences in other bacteria (specifically the closely the hardons and better surviyal in, and adaptation to, the physobora and as vaccine activity and better surviyal in, and adaptation to,
                                                         safe genetic engineering host, allow detection in presence of related bacteria
                                                                                                                                                                                - - - 1
- 1,
                                                   New DNA sequences specific for Pseudomonas
                                                                                                                                                                    Claim la; Page 105-106; 158pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the rhizosphere and soil.
WPI; 2001-192469/20
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Sequence 1581 BP; 284 A; 451 C; 557 G; 289 T; 0 other;

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129 gctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcagga 188
                                                                                                                                                        189 gigiggcaacgaacaaccgcagaacggicaacaggaaggccigagiccgitgacgcagai 248
                                                                                                               985 GCCGGACCACTTGCTCAAGACGTTCCTGCAACGCCTTGGGCGTGCCGTTGAACAGCAGGT 926
                                            Gaps
                                                                                                                                                                                             925 GIGCITCAICGAAGAACAGCGCCAGCACCGGCIIGICGGCAICACCGCGCICGGGCAACI
  Score 37.8; DB 22; Length 1581;
Pred. No. 2.7;
0; Mismatches 77; Indels 0;
                                            ö
                                        .77; Indels
                                                                                                                                                                                                                                                                        865 GCTCGAACAGTTCGGCCAGCACCACAACAGGAACGTCGCG 825
                                                                                                                                                                                                                                    249 gctgatgcagatcgtgatgcagctgatgcagaaccagggcg 289
ch 11.1%;
1 Similarity 52.2%;
84; Conservative
                  Best Local Similarity
Query Match
                                      Matches
                                                                           ò
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Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                        DNA encoding novel human diagnostic protein #15658.
RESULT 7
AAS79854/c
ID AAS79854 standard; cDNA; 4335 BP.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                           40200175067-A2.
                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                         11-0CT-2001
                                                                                              AAS79854;
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DNA sequence of human PPP2R2B

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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase obtain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) as useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. (In polymeride and polymucleotide sequences have applications in claspnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2515 CAGCAGGAGCAGGAGCAGGAGCAGGAGCAGCAGCAGCAGGAGCAG 2456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 cagcagtcgccttcggctggctccgagcagcagctggatcagttgctcgccatgttcatc 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                   mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 atgatgatgctgcaacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 ccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtg
                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4335 BP; 1069 A; 1119 C; 1161 G; 986 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides,
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%; Score 37.8; DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.6;
                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 15658; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2395 CAGCAGCAGCAGCAGCAG 2375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC84677 standard; DNA; 5120 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 atgcagctgatgcagaaccag 285
                                                                                                                             Tang YT
                       31-MAR-2000; 2000US-0540217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 49.3
Matches 99; Conservative
                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                 2001-639362/73
                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                     P-PSDB; ABG15667
                                           23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Microsatellite marker; human; chromosome 5q31-33; D5S402; WI-6763;
CAG trinucleotide repeat; spinocerebellar ataxia 12; SCA12; PPP2RBbeta;
brain; protein phosphatase PP2A; ds.
                                                                                                                                                                                                                                                                                        New polynucleotide for use in diagnosing spinocerebellar ataxia 12
comprises a microsatellite marker having a variable number of CAG
trinucleotide repeats located on human chromosome 5q31-33
                                                                                                                                        /product= ""PPP2R2B""
/note= "protein_id= AAF74024.1"
                                                                                                                                                                                                                                                                                                                         Disclosure; Page 21-23; 23pp; English.
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                  Holmes SE;
                                                                                 "CAG"
                                                                                                                                                                                                16-JUN-2000; 2000WO-US40213.
                                                                2088..2366
/*tag= a
                                                                                 /rpt_type=
                                                                                         .3093
                                                                                                        2473..3023
                                                                                                                 /*tag= c
                                                                                                                                                                                                                                 (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                 /*tag= d
                                                                                                  *tag=
                                                                                                                                                                                                                                                   Ross CA,
                                                                                                                                                                                                                                                                 WPI; 2001-102718/11.
P-PSDB; AAB48340.
                                                                                                                                                                WO200078943-A2
                                                                repeat_region
                                                                                                                                                                                                                                                 Margolis RL,
                                         Homo sapiens
                                                                                                                                                                                                                 18-JUN-1999;
                                                                                                                                                                               28-DEC-2000
                                                                                                        5'UTR
                                                                                        mRNA
                                                                                                                       SDS
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The invention relates to a microsatellite marker located on human chromosome 5q31-33 between markers D5S402 and WI-6763, comprising a variable number of CAG trinuclectide repeats. The marker is useful for diagnosing spinocerebellar ataxia 12 (SCA12) by determining the number of PPD2A parameter is a brain specific regulatory subunit of protein phosphatase PP2A, where if a number greater than 40 ½ determined, an expansion which is associated with SCA12 is indicated. The presence of expanded trinuclectide repeats on chromosome 5q31-33 is useful for predicting or diagnosing SCA12. Also provided are primers useful for amplifying the microsatellite marker associated with SCA12 and for diagnosing SCA12 and proceed on human chromosome 5q31-33. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2045 gaggagectegeetttaatgeaceageegeeteeageeteetgeageageageageagea 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 cgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagcca 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gggcagcgatgcaaatcaggagtgtggcaacgaacaacgcagaacggtcaacaggaagg 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 1336 A; 1267 C; 1268 G; 1249 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%; Score 37.8; DB 22; score 37.8; Pred, No. 3.8; Conservative 0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5120
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9 69 PP

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271 ctgatgcagaaccagggcggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypersensitive response; elicitor; Pseudomonas solanacearum; plant; disease-resistance; Escherichia coli; infiltration; virus; bacterium; fungus; pathogen; biological control agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes a hypersensitive response elicitor from Pseudomonas solanacearum. The elicitor may be used in a new method for imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, leaf abrasion, or plant infection with recombinant bacteria (non-infectious to the host plant, e.g. Escherichia coll) expressing the elicitor as a biological control agent, to alllow recombinant protein infiltration into the plant. The method confers virus, bacterium or fungus disease-resistance on crops and
                             cctgagtccgttgacgcagatgctgatgcagatcgtgatgcagaaccagg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            712 agcgaagaccagggcggcctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg
                                                                                                      gcggcggcatgggcggtggcggttcggtcaacagcagcctgggcggcaac 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - with hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 37.6; DB 18; 55.3%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imparting pathogen resistance to plants response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                       Hypersensitive response elicitor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 51-52; 69pp; English.
                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                    AAT49316 standard; DNA; 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0475775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US08819.
                                                                                                                                                                                                                                           30-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                            Pseudomonas solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-051614/05.
P-PSDB; AAW06600.
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les 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      WO9639802-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imparting
                                                                                                                                                                                                                AAT49316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                    287
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Matches
                                                                                                                                                                        AAT49316
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AAV39975 standard; DNA; 1035 BP

AAV39975

832 aagggtgccggc 843

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Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the control of insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide or protein to control insects on plants or plants grown from seed treated with HRE. Also claimed is a method of insect control for plants that involves: (a) providing a transgenic plant or seed transformed with a DNA molecule (see AAV54606-09) encoding a HRE polypeptide or protein (see AAW75862-67); and (b) growing the transgenic plants or transgenic plants produced from the transgenic seeds to control insects. HRE prevents direct insect damage to plants by feeding injury. It kills insects close to plants, and interferes with insect larval feeding on such plants. It also prevents insects from colonising host plants and releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This DNA sequence comprises an open reading frame that encodes a hypersensitive response elicitor (HRE) (see AAW75865 of Pseudomonas solanacearum. The invention relates to the use of a HRE
                                                                                                                                                                                                              solanacearum hypersensitive response elicitor DNA.
                                                                                                                                                                                                                                                insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ohytotoxins which result in disease damage to plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.6; DE
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                            biological control; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 15; 75pp; English.
                                                                                                                                                                                                                                                elicitor;
                                                                                                            AAV54609 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%;
55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0039226.
                                                                                                                                                                                                                                                                                                                                                                                              98WO-US03604
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.0
Best Local Similarity 55.3
Matches 73; Conservative
                                                                                                                                                                                                                                                                                            seudomonas solanacearum
                                                                                                                                                                                                                                            Appersensitive response
331 ggcggcaacgcc 342
                              832 aagggtgccggc 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-495374/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zitter TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW75865.
                                                                                                                                                                            07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-1997;
                                                                                                                                                                                                                                                                                                                            W09837752-A1
                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                            03-SEP-1998
                                                                                                                                            AAV54609;
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                                                                                           AAV54609
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This DNA sequence comprises an open reading frame that encodes a hypersensitive response elicitor (HEE) (see AAWGA57) of Pseudomonas solanacearum. A method of enhancing growth in plants comprises:

(a) applying a HRE polypeptide or protein in a non-infectious form to a plant or plant seed under conditions effective to enhance growth of the plant or plants grown from the seed, or (b) providing a transgenic plant or plants grown from the seed under conditions of encoding a HRE polypeptide or protein, and growing the transgenic plant or a plant produced from the transgenic seed under conditions of effective to enhance plant growth. HRES (see AAW62454-59) or nucleic acids (see AAW62454-57) encoding them can be used to increase plant growth. THE HES may also result in increased plant height and growth, and effect early germination and maturation of plant seed and early colouration of fruit and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wethod for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g. increase in plant height or earlier germination seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    712 agcgaagaccagggccgcctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg
                                                                                                                      Hypersensitive response elicitor; HRE; growth; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó;
                                                                                Pseudomonas solanacearum hypersensitive response elicitor DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.6; DB 19; Length Pred. No. 2.7;
0; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 21; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                           98WO-US01507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.3%;
Matches 73; Conservative
                                                                                                                                                                                     Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Wei Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 ggcggcaacgcc 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-427940/36.
P-PSDB; AAW62457.
                                                                                                                                                                                                                                                                                                                                                                                                                               Beer SV, Qiu D,
                                                                                                                                                                                                                           W09832844-A1
                                                                                                                                                                                                                                                                                                         27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                 27-JAN-1997;
                                        09-NOV-1998
                                                                                                                                                                                                                                                                   30-JUL-1998
AAV39975;
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Indels

59; DB 19;

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Length 1035;

ctgatgcagaaccagggcggcggcatggggggggggtggcggttcggtcaacagcagcctg 330 772 ctggtgcagatgatgcagcaaggcggcctcggcggcggcaaccaggcgcaggggggctcg 831

ggcggcaacgcc 342

331

271

g ò q AAV83991 standard; DNA; 1035 BP.

RESULT 13 AAV83991

us-09-829-124-1.rng

AAV83991;

(first entry)

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a coding region for a hypersensitive elicitor protein (HRE, see AMW6115). The invention relates to methods of imparting hypersensitive response induced resistance to plants by treatment of seeds. Isolated HRE polypeptides can be applied to seeds as a means of imparting pathogen resistance to plants grown from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erwinia amylovora, Pseudomonas syringae, Pseudomonas solanacearum, Asanthomonas campestris pv. glycines and kanthomonas campestris pelargonii (see AAW61113-18) are provided. The methods can impart pathogen resistance without using agents which are harmful to the environment or pathogenic to the plant seed being treated, or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seeds. Alternatively, bacteria containing the gene encoding the HRE can be applied to the plant seeds, or transgenic plant seeds containing a DNA molecule encoding an HRE polypeptide or protein are used. HRE polypeptide sequences from Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas solanacearum comprises
                                                                                                                                                            Hypersensitive response elicitor; transgenic plant; seed; pathogen resistance; disease resistance; crop protection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Imparting pathogen resistance to plants - by applying hypersensitive response elicitor polypeptide to seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 24-25; 85pp; English.
                                                                                                                                Hypersensitive response elicitor DNA.
                                AAV36430 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                         (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide sequence from
                                                                                                                                                                                                                                                                                                                                              96US-0033230.
                                                                                                                                                                                                                                                                                                            97WO-US22629
                                                                                                 (first entry)
                                                                                                                                                                                                               Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-332931/29.
                                                                                                                                                                                                                                                                                                                                                                                                            Beer SV, Qiu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW61116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adjacent plants.
                                                                                                                                                                                                                                                                                                            04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                          05-DEC-1996;
                                                                                                26-OCT-1998
                                                                                                                                                                                                                                                                            11-JUN-1998.
                                                                AAV36430;
 12
RESULT 1
AAV36430
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211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
                                                                           712 agcgaagaccagggcgctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg 771
                            0;
     DB 19; Length 1035;
                            59; Indels
 11.0%; Score 37.6; DB
55.3%; Pred. No. 2.7;
ive 0; Mismatches
             Best Local Similarity 55.3
Matches 73, Conservative
                                                                                                                                                         331 ggcggcaacgcc 342
                                                                                                                                                                                   aagggtgccggc 843
Query Match
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The present sequence encodes a hypersensitive response elicitor protein (also called hairpin protein) that is able to elicit a hypersensitive response in plants. The specification also describes hypersensitive response elicitors from other pathogenic organisms. The protein, in non-infectious form, is applied to plants to impart disease resistance (to a wide range of viral, bacterial and fungal pathogens), to improve growth (yield, quantity and quality of seeds, to provide earlier germination etc.) and to control insects (e.g. corn borers, Lepidoptera larvae etc.) The same results are provided by transgenic plants expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fragments of an Erwinia hypersensitive response elicitor protein and related DNA - used to impart disease resistance to plants, to increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= Hypersensitive_response_elicitor_protein
                                               Hypersensitive response elicitor protein; hairpin protein; disease resistance; seed quality; insect control; corn borer; Lepidoptera larvae; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1035;
DNA encoding a hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37.6; DI
Pred. No. 2.7;
0; Mismatches
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                                                                                                                                                                                                        Location/Qualifiers
1..1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORR ) CORNELL RES FOUND INC. (EDEN-) EDEN BIOSCIENCE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US10874.
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55.3%;
                                                                                                                                                         Pseudomonas solanacearum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-070210/06.
P-PSDB; AAW87641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laby RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAY-1998;
                                                                                                                                                                                                                                                                                                                                  WO9854214-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1997;
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/*tag= a /product= "hypersensitive response elicitor protein"

Location/Qualifiers 1..1035

/*tag=

WO200020452-A2.

Pseudomonas solanacearum.

ornamental plant; ss.

Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; crop;

DNA encoding a hypersensitive response elicitor protein.

08-AUG-2000 (first entry)

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The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a DNA encoding hypersensitive response elicitor protein from Pseudomonas solanacearum. The present sequence is used to transform transgenic plant or plant seeds to impart stress resistance.
                                                                                                     Pseudomonas solanacearum hypersensitive response elicitor encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application of a hypersensitive response elicitor protein to plants impart stress resistance
                                                                                                                                   Hypersensitive response elicitor; environmental stress resistance;
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                                                                                                                                                                                                                                /*tag= a
/product= "Hypersensitive response elicitor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37.6; DB 21;
Pred. No. 2.7;
0; Mismatches 59;
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1..1035
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 28; 84pp; English.
                          AAD00674 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                            (EDEN-) EDEN BIOSCIENCE CORP.
                                                                                                                                                                                                                                                                                                                          99WO-US26039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 11.0%;
Best Local Similarity 55.3%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                   98US-0107243
                                                                              (first entry)
                                                                                                                                                                          Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                       Schading RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376566/32.
P-PSDB; AAY71099.
                                                                                                                                                                                                                                                                     WO200028055-A2
                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998;
                                                                            08-SEP-2000
                                                                                                                                                                                                                                                                                                                        04-NOV-1999;
                                                                                                                                                                                                                                                                                               18-MAY-2000.
                                                   AAD00674;
                                                                                                                                                                                                                                                                                                                                                                                                        Wei Z,
RESULT 14
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Fan H, Niggemeyer JL;

Wei Z,

WPI; 2000-303745/26. P-PSDB; AAY84860.

(EDEN-) EDEN BIOSCIÈNCE CORP.

99WO-US23181. 98US-0103050.

05-OCT-1999; 05-OCT-1998;

13-APR-2000.

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polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the proteins impart disease resistance to plants, caponse. Instead, the proteins impart disease resistance to plants, cannot plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parsnip, turnip, cauliflower, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, prape, raspberry, prape, raspberry, prape, control, sorghum or sugarcane, arbidopsis thaliana, saintpaulia, comato, sorghum or sugarcane, arbidopsis thaliana, saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 agcgaagaccagggcggcctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants, especially vegetables and ornamental flowers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag
                                                                                                                                                                                                                               The present sequence encodes a hypersensitive response elicitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1035 BP; .227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                 Disclosure; Page 29-30; 100pp; English.
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Best Local Similarity 55.35
Frac 73; Conservative
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Indels

AAA14944 standard; DNA; 1035 BP

RESULT 15 AAA14944 ID AAA1494 XX AC AAA1494

AAA14944;

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Search completed: June 28, 2002, 11:25:04 Job time: 3736 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Com

nucleic search, using sw model

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,254
FILING DATE: 10-JUL-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Induced Resistance In Plants
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Pred. No. 0.19;
                                                                                                                  US-08-459-448A-4
US-08-459-448A-4
US-08-459-595A-2
US-08-459-595A-4
US-08-459-504B-2
US-08-459-504B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                   PCT-US92-03222-44
                                                                                                                                                                                                                                                                                                                     US-09-053-549-3
US-09-053-549-5
                                                                                                                                                                                                                                                                                                                                                                                            US-09-547-422-4
US-09-292-768-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08891254
Patent No. 5776889
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%;
55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1035 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 55.3.
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U.S.A.
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US-08-891-254.-8
                                           US-08-891-254-8
June 28, 2002, 10:22:23 ; Search time 39.55 Seconds (without alignments) 2124.062 Million cell updates/sec
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Sequence 1132, A
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Patent No. 5
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Sequence 67
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                                      Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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hits satisfying chosen parameters:

of

Total number

Searched:

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Issued_Patents_NA;*

383533 seqs, 122816752 residues

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

US-09-829-124-1

Perfect score:

Sequence:

Scoring table:

US-08-425-069-1 US-08-317-844B-1 US-09-103-840A-2 US-08-998-416-1132

PCT-US96-08819-8

US-09-030-270A-8 US-08-984-207-8 US-09-013-587-8

SUMMARIES

ВВ

Length

Query Match 1

Result Š US-09-292-768-69 US-08-276-452A-72 US-08-798-744-72

US-09-292-768-67

1665 1665 1665 1665

US-08-881-784-8 US-09-292-768-3

US-09-056-556-221

JS-09-253-691-3

US-08-317-844B-3

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832 AAGGGTGCCGGC 843
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                                                       RESULT 3
JS-09-030-270A-8
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271 ctgatgcagaaccagggcggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330
                                                                                                 772 CTGGTGCAGATGATGCAGCAAGGCGGCCTCGGCGGCGCAACCAGGCGCAGGGCGCGGCTCG 831
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NDTA:
APPLICATION NUMBER: US/08/819,539
FILING DATE: 17-MAR-1997
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.0%; Score 37.6; DB 2;
55.3%; Pred. No. 0.19;
tive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                          E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
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                                                                                                                                                                                                                                                     Sequence 8, Application US/08819539 Patent No. 5859324 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727
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APPLICANT: Beer, Steven V
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CORRESPONDENCE ADDRESS
                                                                                                                                  331 ggcggcaacgcc 342
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Best Local Similarity
Matches 73; Conserv
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US-08-819-539-8
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271 ctgatgcagaaccagggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330
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                                                                   APPLICANT: Zitter, Thomas A.
APPLICANT: Wei, Zhong-Min
TITLE OF INVENTION: INSECT CONTROL WITH A
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
                                                                                                                                                                                                               E: Nixon, Hargrave, Devans & Doyle LLP
P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,270A
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Pred. No. 0.19
0; Mismatches
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Sequence 8, Application US/09030270A Patent No. 5977060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.3%;
Matches 73; Conservative
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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Wei, Zhong-Min
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EDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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CORRESPONDENCE ADDRESS:
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                                             GENERAL INFORMATION:
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APPLICANT: Q1u, De
APPLICANT: We1, Z1
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                          SEED TREATMENT
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APPLICANT: Qiu, Dewen
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square CITY: Rochester
                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: Clinton Square, P.O. Box 1051
   HYPERSENSITIVE RESPONSE RESISTANCE IN PLANTS BY
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Pred. No. 0.19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET UNMBER: 19603/1201
TELECOMMUNICATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,230
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,207
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; MOLECULE TYPE: DNA (genomic)
US-08-984-207-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.33
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid_
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                               New York : U.S.A.
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                                                                                                                                                 COUNTRY:
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211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             712 AGGGAAGACCAGGGCGCCTCACCGGCGTGCTGCAAAGCTGATGAAGATCCTGAACGCG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     772 CTGGTGCAGATGATGCAGCAAGGCGGCCTCGGCGGCGGCGAACCAGGCGCAGGGCGGCTCG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37.6; DB 4; Length 1035;
Pred. No. 0.19;
0; Mismatches 59; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application PC/TUS9608819
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
TITLE OF INVENTION: RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/n1?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                   19603/1501
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,048
FILING DATE: 27-JAN-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,775
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1035 base pairs
COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                 NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic)
JS-09-013-587-8
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Best Local Similarity 55.3%;
Matches 73; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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APPLICANT: Lewis, Randolph V.

APPLICANT: Xu, Ming

APPLICANT: Xu, Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND A TRANSFORMED CELL

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 ctgatgcagaaccagggcggcggccggcatgggcggtggcggttcggtcaacagcagcctg 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 AGCGAAGACCAGGGCGGCCTCACCGGCGTGCTGCAAAAGCTGATGAAGATCCTGAACGCG 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1035;
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                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Birch, Stewart, Kolasch & Birch
: 301 No. 5728810th Washington Street
Falls Church
Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                Score 37.6;
Pred. No. 0.
                                      NAME: Goldman, Wichael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/10051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1447-106P
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FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08425069
Patent No. 5728810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                      TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1035 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                            11.0%;
ilarity 55.3%;
Conservative
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                          single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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Best Local Similarity
Matches 73; Conserv
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110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagg 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           579 ACAAGGAGGCTATGGAGGACTTGGAAGCCAAGGTGCTGGACGAGGAGGATTAGGTGGACA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcg 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639 AGGIGCAGGAGCAGCAGCAGCAGCAGCIGGAGGIGCCGGACAAGGAGGACIAGGIGG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOLATED DNA CODING FOR SPIDER SILK
PROTEIN, A REPLICABLE VECTOR AND A TRANSFC
CONTAINING THE ISOLATED DNA, AND PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%; Score 37.2; DB 1; Length 2338; 49.5%; Pred. No. 0.33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1: FROM 1 TO 2338
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street CITY: Falls Church STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                     AUTHORS: Xu, Ming AUTHORS: Lewis, Randolph V. TITLE: Structure of a protein superfiber: JTITLE: draffine silk JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                          /product= "Nephila cladragline silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08317844B Patent No. 5989894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Au, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DN.
TITLE OF INVENTION: CONTAINING THILE OF INVENTION: CONTAINING THUBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kol
                                                                                                  ORIGINAL SOURCE:
ORGANISM: Nephilia clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1.2154
OTHER INFORMATION: 4rag
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 49.5
Matches 96; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                               MOLECULE TYPE: CDNA
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OPERATING SYSTEM:
                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                             7120-7124
                                                                                                                                                                                                                                                                                                                                                TITLE: drain
JOURNAL: Pro
                                                                                      HYPOTHETICAL:
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Db 2543256 TTGGCTACCACCATGCGAGGGGGAGCGCCGACCGCACGGAGGTAG 2543197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 2543196 CCCGGTGTGGGGTGACGGGCCAATGGCAGGTGCCGGCGATGGCGCGATCCGCCTGCTGC 2543137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 2543076 ACCTGGCGTGCGCGGGGATCGTCAGTTCCGGGACGAGCTGCACCAGGGGGACCGCCGCG 2543017
                                                                                                                                                             OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 cgccttcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatga 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 tgctgcaacagagccagggcagcgatgcaatccaggagtgtggcaacgaacaaccgcaga 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 acggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagc 271
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                             32 teggeaacetgeagaegatgggeategggeeteageaacaegaggaetecagecageagt 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.4; DB 4; Length 4403765;
Pred. No. 6.1;
0; Mismatches 161; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6239264artis Corporation
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                                                                                                                  ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1132, Application US/08998416
; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Philippsen, Peter
                                                                                                                                                                                                                                                                                                   Query Match 10.6%;
Best Local Similarity 45.2%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pohlmann, Rainer
Steiner, Sabine
                            SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Philip
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                                               SEQ ID NO 2
LENGTH: 4403765
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US-08-998-416-1132
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APPLICANT:
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                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 gcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcc 229
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General INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: FROM 1 TO 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Nephila clavipes dragline silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure of a protein superfiber: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A
                                                              NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REPERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..2154 OTHER INFORMATION: /product=OTHER INFORMATION: dragline spublication information:
                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Nephilia clavipes
                                                                                                                                                                                                   TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Ku, Ming AITHORS: Lewis, Randolph V.
04-OCT-1994
                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                    (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.9°
Best Local Similarity 49.5°
Matches 96; Conservative
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FILING DATE: 04
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL: N
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JOURNAL: Prc
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                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-949-155-5
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                                                                        LENGIH:
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                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 gagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccag 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 ggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggc 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 GAGAAGGAGCTGGCGATGCTGGACAAGCTGCTGGAGAAGACGACGGGGGGGACAAACCAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 GCGCTGAAGCAGACGATGGTGTCTGACGAACTTCGCGCGGTTCCGGGACCAGGAGACG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcaga 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/949,155 FILING DATE: Concurrently Herewith
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMONICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ARNOLD, WHITE AND DURKEE STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 5, Application US/08949155
; Patent No. 6271436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1132:
                                                                                                                                                                                                            ..rology: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

CORGANISM: PAG1689UP

US-08-998-416-1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (512) 418-3000
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 657 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                        87; Conservative
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IOR APPLICATION DATA:
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Best Local Similarity
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106 tecgageageagetggateagttgetegeeatgtteateatgatgatgetgeaacagage 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 ATAGAGGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGCTGGAGGCGCAGCTGGGC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 ggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccag 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 4; Length 1126;
Pred. No. 0.54;
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ADDRESSEE: christensen, O'Connor, Johnson and Kindness ADDRESSEE: PLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                            0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
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FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/881,784
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Patent No. 6083731
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Shelton, Dennis K. REGISTRATION NUMBER: 26,997
                                                                                                                                                                                                                                                             10.5%;
milarity 49.0%;
Conservative 0
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TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Croteau, Rodney
APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: THE PRO
                                         : 1126 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1665 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 GTGGGCGCGACATGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 ggcggcgccggcatgg 301
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INFORMATION FOR SEQ ID NO:
                                                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 96; Conserv
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                                                            TYPE: nucleic
STRANDEDNESS:
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APPLICANT: Croteau, Rodney B
APPLICANT: Luplen, Shari L
APPLICANT: Muplen, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: LIMONEN HYDROXYLASES
FILE REFRENCE: waurila463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
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                                                                                                                                                                                                                   85 ATCAAGCAATGGCGAAAACCGAAACCCCAAGAACCTGCCTCCGGGCCCGCCGAAGCTG 144
                                                                                                                                                                                                                                                                               Cagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagc 174
                                                                                                                                                                                                                                                                                                                                         175 gatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagt 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ccgctgatcgggcacctccacctcctatgggggaagctgccgcagcacgcgctggccagc 204
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                                                                                                                                                                                                                                                                                                    235 ccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcgcgc
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                                                                                                                                                           Length 1665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 ggcatgggcggtggcggtccaacagcagcctgggcggcaacgcc 342
                                                                                                                                                                      Pred. No. 1;
0; Mismatches 158; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.2; DB 4;
Pred. No. 1;
); Mismatches 158;
                                                                                                                                                         DB 3;
                                                                                                                                                           Score 35.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/09292768
; Patent No. 6194185
                                                          ORGANISM: Mentha x piperita INMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                       10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.3%;
Best Local Similarity 45.1%;
Matches 130; Conservative
                                                                                                                                                 Query Match 10.3
Best Local Similarity 45.1
Matches 130; Conservative
   single
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                           MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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; LOCATION: (19)..(1518)
US-09-292-768-3
                linear
STRANDEDNESS:
                                                                                       US-08-881-784-8
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US-09-292-768-3
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APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
                                                                                                                                                    265 ctctcgtcccgcgaggccacgaaggaggcgatgaagctggtggacccggcctgcgcggac 324
                                                   205 giggingaagcagtanggeecagiggegeangigeagetenggegaggigitetenging 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 cogetgategggeacetecacetectatgggggaagetgeegeageagegggggeage 204
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OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase variant
175 gatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagt
                                                                                                    235 ccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcgcc
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Pred. No. 1;
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CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67, Application US/09292768 Patent No. 6194185 GENERAL INFORMATION:
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Best Local Similarity 45.1%;
Matches 130; Conservative
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; LOCATION: (19)..(1518)
US-09-292-768-67
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LENGTH: 1665
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TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
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OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase protein variant
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OTHER INFORMATION: limonene-3-hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 158;
                                                                                                                                                                                              FILE REFERENCE: wsur13463
CURRENT APPLICATION NUMBER: US/09/292,768
                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
Sequence 69, Application US/09292768
Patent No. 6194185
                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Seguence
                                           GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
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Best Local Similarity 45.1
Matches 130; Conservative
                                                                                                Lupien, Shari L
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US-09-292-768-69
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Search completed: June 28, 2002, 11:27:18 Job time: 3895 sec

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(without alignments)
2877.941 Million cell updates/sec
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                                                                                                    June 28, 2002, 10:21:28 ; Search time 1603.91 Seconds .
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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342
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_pln:* em_gss_vrt:*

gb_est2

qb_est1

gb_gss:

em_esthum: em_estba:* em_estin:

em_estov

em_estp]

Description	AZ312601 1M0028104 BG930118 ets4BEST05 AQ919110 RPCI-23-2 BB867074 BB867074 AL241091 Tetracdon B1895704 EtESTed23 AZ101123 RPCI-23-4 BG929756 ets4BEST01 AZ661219 1M0539M10 B1822289 603080137 AU142497 AU142497 BG417526 HYSMEK01 BF592443 7156C04.x AZ640388 1M0502E21 BF199083 249143 MA AZ337339 1M0068B03 BG562218 EtESTee04
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& Query Match	12.2 12.2 12.2 12.2 12.2 12.2 11.3 11.9 11.8 11.7 11.5 11.5
Score	44444444444444444444444444444444444444
Result No.	C C C C C C C C C C C C C C C C C C C

c 18		11.4	821	10	BF570046	BF570046 60218605
19	œ	11.3	546	6	AJ273961	161 A.T.27.3961
20	8	11.3	650	10	· BM488443	•
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c . 22	38.6	11.3	718	17	A2972907	A2977907 7M0246W24
23	æ	11.2	1006	12	CNS04S5P	
24	œ	11.2	541	12	B73805	C
25	38	11.1	330		BG560855	
56	38	11.1	354		BB870603	
c 27	38	11.1	501		AI366107	
78	38	11.1	615	О	AW106297	AW106297 um25h04.v
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	37.8	11.1	812	13	CNS03U05	
	37.8	11.1	1042	12	CNS04N1V	
	37.6		840	6	AL669315	
		•	609	10	BI633649	6
	37.4	10.9	822	10	BG299472	
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c 41	37.2	٠.	348	σ,	AI440942	
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£.3	٠		440	0	BI895386	95386
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45	•		473		AW277347	1347
					ALIGNMENTS	
RESULT 1						
AZ312601/c					,	
LOCUS	AZ312601	2601		;	526 bp DN	linear GSS 29-SEP-200
DEFINITION	1M00,	IMO028I04R Mouse 10k	Mouse 1	10kb	plasmid UUGC1M	library Mus muşculus genomic
ACCESSION	AZ312601	2601				
VERSION KEYWORDS	AZ312601	2601.1	GI:10356717	1567	17	
SOURCE	house	house mouse				
ORGANISM	Mus	Mus musculus	. 02			
	Eukar	vota:	Metazoa		Eukaryota: Metazoa: Chordata: Craniata: Vertebrata:	Vertebrata: Enteleostomi:

LOCUS	AZ312601 526 bp DNA linear GSS 29-SEP-2000
	clone UUGC1M0028104 R, DNA sequence.
ACCESSION	AZ312601
VERSION	AZ312601.1 GI:10356717
KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Chordata;
	Rodentia;
REFERENCE	
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
	:
	/M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
	and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
	plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss
	University of Utah Genome Center
	University of Utah
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC. ITT
	84112, USA
,	Tel: 801 585 5606
	Fax: 801 585 7177
	Email: ddunn@qenetics.utah.edu
	Insert Length: 10000 Std Error: 0.00
-	Plate: 0028 row: I column: 04
2	Seq primer: CACACAGGAAACAGCTATGACC
	Class: plasmid ends
	High quality sequence stop: 526.
FEATURES	Location/Qualifiers
sonrce	1526
	/organism="Mus musculus"
	/scrain="c3/BL/6J"
	/db_xref="taxon:10090"
	/clone="Underlands28104" /clone lib="Wouse 10bb plasmid mrc111 lib=
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AQ919110
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                                                                                   FEATURES
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                                                                         (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgc 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 aaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgtt 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43.8; DB 12;
Pred. No. 3.7;
0; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Centre for Gene Analysis and Technology
Universiti Kebangsaan Malaysia
43600 UKM Bangi, Selangor DE, Malaysia
Tel: 6 03 829297
Fax: 6 03 829249
                                                            Laboratory Mouse DNA Resource
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Eimería tenella
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571 bp DNA linear GSS 21-DEC-1999
-RFCI-23-275E22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-275E22
A0919110
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 571)
                                                                                                                                                                                                                                                                                                                               /note="Vector: Lambda ZAPII; Site_1: EcoRI; Site_2: Xhoi Sporozoites were excysted in vitro from E. tenella H occysts, purified by column chromatography and mRNA extracted using a FASTTRACK kit (Invitrogen). cDNA was synthesised and a Uni-ZAP XR library was constructed using cDNA synthesis kit, ZAP-CDNA synthesis kit and ZAP-CDNA synthesis kit and Lapracy was amplified once through E. coli XLI-Blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 tcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctg 156
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Unpublished (1999)
Other_GSSs: RPCI-23-275E22.TV
Coherct: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.8; DB 10;
Pred. No. 10;
0; Mismatches 127;
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    537
    /organism="Eimeria tenella"
/strain="Houghton"
/db_xref="taxon:5802"

                                                                                                                                                                                                                                       /clone="etsHk077"
/clone_lib="EtH11"
/dev_stage="Sporozoite"
/lab_host="XL1-Blue MRF""
Email: klwan@pkrisc.cc.ukm.my
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 g
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Matches 118; Conservative
                   PCR PRimers
FORWARD: T3
BACKWARD: T7
Seq primer: SK.
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51 AACTGCAGCAGGAGCTCCTGGTCCTCAAGCAGCAGCAGCAGCTCCAGAAGCAGCTCCTGT 110
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Best Local Similàrity
Matches 136; Conserv
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COMMENT
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ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI wethylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BHIOB electrocompetent cells (BRL Life Technologies).

112 c 142 g 55 t
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                                                                Email: szkodétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SPG
Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 aacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtc
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       9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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 Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.2%; Score 41.6; 48.0%; Pred. No. 12
                                                                                                                                                                                                                                                                                     /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                            /clone="RPCI-23-275E22"
                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                     Location/Qualifiers
Genomic
                                                                                                                                                                                                                                                                                                                                                                                               /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                        /strain-"C57BL/6J
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Best Local S
Matches 119
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ORIGIN
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Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tito, M., Kaval, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Makamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, T., Okido, T., Saito, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tonaru, A., Toyari, Watchiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RKEN full-length enriched, pooled cell lines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper.selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepare full length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (strain=C3H, tissue_type=brain, cell_line=CRL-1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
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Pred. No. 14;
0; Mismatches 158;
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/clone="G4D0005H22"
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Indels

289 GCCAGACCAGGASCCAGACCASBHYCCAGACCAGGACCAGACCAGAGCAGGA 230 gotggatcagttgotcgccatgttcatcatgatgatgctgcaacagagccagggcagcga 176

117

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177 tgcaaatcaggagtgtggcaacgaacaccgcagaacggtcaacagga

BI895704 425 bp mRNA linear EST 15-OCT-2001 EtESTed23h03.yl Eimeria tenella S5-2 cDNA Neg Selected Elmeria tenella cDNA 5', mRNA sequence.

DEFINITION

BI895704

ACCESSION VERSION KEYWORDS SOURCE

BI895704.1 GI:16138840

Eimeria tenella. Eimeria tenella

ORGANISM

Eimeria.

REFERENCE AUTHORS

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;

Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R., Wilson, R. and Sibley, D. Unpublished (1999)

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CNSO3FOQ 968 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 021M15 of library G from Tetraodon nigroviridis, genomic survey
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 968)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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1 (bases 1 to 968)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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t 56 others
231 GGCAGCGGGAGCAGCAGCGGCAGGAGCTGGAGAAACAGCGGCTGGAGCAGCAGCTGC 290
                                                                                       aacagagccaggggcagcgatgcaaatcaggagtgtgggcaacgaacagccgcagaacggtc
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Tetraodon nigroviridis.
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Email: est@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
Information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco
High quality sequence stop: 391.
Location/Qualifiers

/organism-"Eimeria tenella"

source

FEATURES

MO 63108, USA

Contact: David Sibley, Ph.D.
WashU-Merck Elmeria tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1800

TITLE JOURNAL

COMMENT

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/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Sporozoites were obtained from in vitro sporulated and
excysted oocysts of E.tenella grown in chickens. CDNA was
synthesized from poly mRNA using an oligo-dT primer
containing a XhoI site. Following second strand synthesis,
EcoRI adapters were ligated to the CDNA and products were
slace-selected on sephacryl S500. The CDNA were ligated to
ECORI/XhoI prepared lambda Zapii (Stratagene). Clones were
converted to phagemids by mass excision using ExAssist
helper phage and E.coli Solx cell (Stratagene). Clones
were selected by negative hybridization against a pool of
overrepresented ESTS (N>-10, from 1682 previous reads).
Insert sizes range from 1.2-2.9Kb. The library may contain
a small percentage of host or bacterial contaminents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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Pred. No. 17;
0; Mismatches 112;
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51.3%;
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Matches 119; Conservative
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Gaps

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72; DB 12;

12.0%; Score 41.2; Di 41.1%; Pred. No. 17; :ive 27; Mismatches

Conservative

Query Match Best Local Similarity Matches 69; Conserv

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Length 968; Indels

egggcetcagcaacacgaggaettccagccagcagtegcettcggetggetccgagcagca 116

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70 cacgaggactccagccagcagtcgccttcggctggctccgagcagcagctggatcagttg 129
                                                                                                                   130 ctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcaggag 189
                                                                                                                                                                                                  132 CAGCAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAG 191
                                                                                                                                                                                                                                          190 tgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatg 249
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AUTHORS
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KEYWORDS
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803 bp DNA linear GSS 09-MAY-2000 RPCI-23-478E19 TJ RPCI-23 Mus musculus genomic clone RPCI-23-478E19
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Ehao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, J., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu, Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu,orderingframe.htm) or from Resea ch Genetics (info@resqen.com). BAC end page: http://www.tigr.org/tdb/Dac_ends/mouse/bac_end_intro.html Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Size
  176 CGCTAGCAGCACCAGCAGCAGCAGCAGCAGCAGCCGCTAGCAGCAGCAGCACCAG 235
                                                                                 229 ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-g 287
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                                                                                                                                                                                              288 cggcgccggcatgggcggtggcggttcggtcaacagcagcctggggcgaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Chrez-GSSs: RRCI-23-478E19.TV
Contact: Shaying zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
711: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                    AZ101123.1 GI:7754179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .803
                                                                                                                                                                                                                                                                                                                                                       , DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse
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ORIGIN
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AUTHORS
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BG929756 325 bp mRNA linear EST 31-DEC-2001 etsHEST0177 EtH11 Eimeria tenella cDNA clone etsHd066 5', mRNA
                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimerlida; Eimerlidae;
                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 325)
Ng.S.T., Jangi,M.S., Shirley,M.W., Tomley,F.M. and Wan,K.L.
Comparative EST analyses provide insights into gene expression in
two asexual developmental stages of Eimeria tenella
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: Lambda 2APII; Site_1: EcoRI; Site_2: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sporozoites were excysted in vitro from E. tenella Hoocyste, purified by column chromatography and mRNA extracted using a FASTRACK kit (Invitrogen). CDNA was synthesised and a Uni-ZAP XR library was constructed. using cDNA synthesis kit, ZAP-CDNA synthesis kit and ZAP-CDNA Glapack III Gold cloning kit (Stratagene). The library was amplified once through E. coli XIJ-Blue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.6; DB 10;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centre for Gene Analysis and Technology
Universiti Kebangsaan Malaysia
43600 UKM Bangi, Selangor DE, Malaysia
Tel: 6 03 8292997
Fax: 6 03 8293249

    325
    /organism="Eimeria tenella"
/strain="Houghton"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Sporozoite"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5802"
/clone="etsHd066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: klwan@pkrisc.cc.ukm.my
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                 BG929756.1 GI:18003146
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51.5%;
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                                                                                                                                                                                                                                                                                                           tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wan KL
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BACKWARD: T7
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ORIGIN
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Indels

Length 803;

DB 12;

Score 40.8; DB 12; Pred. No. 20; 0; Mismatches 147;

11.9%; 46.7%;

Query Match 11.9 Best Local Similarity 46.7 Matches 129; Conservative

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Best Local Simi
Matches 120;
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BI832289
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 559)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A.; von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                               230 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-gc 288
                                           110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagg 169
                                                                                                                                    170 gcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcc 229
                                                                                                                                                                                  99 AGAGGCAGCAGCAGCAGCAGCGGCACCAGCAACTGCAGCTGCAACAAAACAGCTGGTGC 158
                                                                        39 AGCAGCAGCAGCAGCAGCAGCAGCTGCCTTTGCTGCAGCAGCTACTGCAGATTCCCTAG 98
                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library
  Indels
                                                                                                                                                                                                                                                                                                                           289 ggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcgg 335
                                                                                                                                                                                                                                                                                                                                                     Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0539 row: M column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0539M10"
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  Conservative ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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of pWD42 (gi[4732114|gb|AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplialin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
blarzyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 585)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov.j column: 10
Plate: LLAM11477 row: j column: 10
High quality sequence start: 8
High quality sequence stop: 375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 gagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaacca-ggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 cggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcggcaacgcc 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                   Length 559;
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Pred. No. 20;
0; Mismatches 114;
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/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="IMAGE:5171817"
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                                                                                                                                                                                                                                                                                                                             11.9%;
llarity 51.1%;
Conservative
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B1832289
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Gaps

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86;

Mismatches

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Conservative

92;

Matches

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116 agctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcg 175

371 AGCACAATGACTTTCTGAAGCTGAGAACCATGCTCATGAAAGTGGAGAATGAGGACATGA 430

236 cyttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcgc 293

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0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHH MGC Library."
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.5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 815)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                         cyccatyttcatcatgatgatgctycaacagagccagggcagcgatgcaaatcaggagtg 191
                                                                                                                                                                                                                                                    45 CCCCCTTGTTGTTATGAAGGAAACGGAAGACTCCGGGCCGAGGAGGCGAAGAGA 104
                                                                                                                                                                                                                                                                                              192 tggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatgct 251
                                                                                                                                                                                                                                                                                                                                 105 AGGAAGGAGGGTCGGAGGACGACGAGGACAACCAGAGGCCGCTGGAGGACAGCGC 164
                                                                                                                                                                                                                                                                                                                                                                                                       165 GACGGAGGCGAGGAGCCCCCGCGGGTAGCGGAGGAGGCGCGAAGGCCGCGAGGGCGCTC 224
                                                                                                                                                                                                                                                                                                                                                                      252 gatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatgggcggtggcgg 311
                                                                                                                                                                                            Gaps
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                                                                                                                                                     Length 585;
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1532–3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                                               Score 40.4; DB 10;
Pred. No. 22;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Y79AA1"
/cell_type="retinoblastoma"
/cell_line="Y79"
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209 d
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/db_xref="taxon:9606"
/clone="Y79AA1000431"
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                                                                                                                                                   11.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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                                                                                                                                                                                    101; Conservative
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BG417526 850 bp mRNA linear EST 23-OCT-2001
HVSMEk0017024f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0017024f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; Plants were raised from seeds in a Controlled Environments growth chamber maintained in continuous light at 180c, and testa and periodarp were dissected from developing kernels at Washington State University, Pullman, WA (Kannangara, von Wetstein). Total RNA was prepared, poly(A) RNA was purified, one CDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TY close lab at the University of California, Riverside (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang). Phagemids were plated and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases I to 850)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., von
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., von
Wetstein, D., Akhunov, B., Chin, A., Chol, D.W., Fericon, R.D., Kianian
P., Otto, C., Simons, K., Zhang, D., Begum, D., Frisch, D., Yu, Y.
Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D.
Bevelopment of a genetically and physically anchored EST resource
for barley genomics: Morex testa/pericarp cDNA library
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rambo, Main). The sequence has been trimmed to remove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Hordeum vulgare testa/pericarp EST library HVcDNA0013 (normal)"
SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="testa/pericarp"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute

    850
    /organism="Hordeum vulgare"
/cultivar="Morex"

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/clone="HVSMEk0017024f"
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100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                            GI:13323077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rotal hq bases = 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare
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BG417526.1
                                                                                                                                                                                                                                                                                  sequence.
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Length 815;

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Score 40.4; I Pred. No. 24;

11.8%; 51.7%;

Query Match Best Local Similarity

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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dennis Sgroi, M.D., Kristina Cole, M.D., Ph.D.
student, Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Rashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
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vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hòminidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 291)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                         152 tgctgcaacagagccagggcagcgatgcaatcaggagtgtggcaacgaacaaccgcaga 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 acggicaacaggaaggccigagiccgiigacgcagaigcigaigcagaicgigaigcagc 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TGAAGCCACAGAAGGCCAGTGGGTGCATTCGCAGTGGCGGAACGGCGACACTCACA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 tgatgcagaaccagggcggcgccggcatgggcggtggcggttcggtcaacagcagcctgg 331
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0
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                                                                                                                                                                                                                                                                                                                                                                                            91;
                                                                                                                                                                                                                                                                                                                                         Score 40.4; DB 10;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Seg primer: -40RP from Gibco.
Location/Qualifiers
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/lab_host="DH10B"
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BF592443
BF592443.1 GI:11684767
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51.1%;
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Best Local Similarity 51.1
Matches 95; Conservative
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carcinoma tissue, cDNA made by oligo-dr priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 400 bp. Primary library,
non-amplified. "
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 605)
10 (bases 1 to 605)
11 (bases 1 to 605)
12 (bases 1 to 605)
13 (bases 1 to 605)
14 (bases 1 to 605)
15 (bases 1 to 605)
16 (bases 1 to 605)
17 (bases 1 to 605)
18 (bases 1 to 605)
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was hydrodynamically sheared by repeated passage through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, 0SA
1711: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 gcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccaggg 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 GAAGCAGGAGGAGCAGATGCGGAAGCAGGAGCAGATGGGGGGAGCAGGAGGAGCAGAT 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Insert Length: 10000 Std Error: 0.00
Plate: 0502 row: E column: 21
                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 1
Pred. No. 23;
0; Mismatches
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    .605
    /organism="Mus musculus"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0502E21"
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51.7%;
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us-09-829-124-1.rst

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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oilgonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 K range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114|gb|AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaa&agagccagg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcc 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-gc 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39.8; DB 12; Length 605;
Pred. No. 31;
0; Mismatches 112; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 ggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcggcaac 339
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Best Local Similarity 51.1%;
Matches 118; Conservative
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Search completed: June 28, 2002, 10:50:23 Job time: 1735 sec
                                                            EST 03-NOV-2000
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FOR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                   Smith, T.P.L., Casas, E.,
                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Cranlata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                       Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                             briyy083
249143 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
Bri99083
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                   Rohrer, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                 1 (bases 1 to 507)
Fahrenkrug, S.C., Freking, B.A., Stone, R.T., Heaton, M.P., Grosse and Keele, J.W.
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Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 507
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                                                                                                              BF199083.1 GI:11090834
                                                                                                                                                                               scrofa
    BF199083/c
LOCUS
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ACCESSION
                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
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COMMENT
                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                       TITLE
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FEATURES

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/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                                      cagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggc 171
                                                                                                                                                                                                                                                                                                                                                                                           307 CACCAGCTGGGTCAACCCCAGGCCTAGGGCTTGGCGCTCCTGCTGGTCACGCTCCAGGGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                              172 agcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctg 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 GG-CAGGCGCTCACAAGCCATGACCCTTACTGGTGGAGCTGGGGCCTCGCATGGGCCAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 agtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggc 291
                                                                                                                                                                                                                    Length 507;
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                                                                                                                                                                                                                 Score 39.2; DB 10;
Pred. No. 40;
0; Mismatches 128;
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_llb="MARC 2PIG"
                                                    /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                 11.5%;
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June 28, 2002, 10:16:03; Search time 23.71 Seconds (without alignments) 534.054 Million cell updates/sec
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584
1 MDSIGNNFSNIGNLOTMGIG.......OGGAGMGGGGSVNSSLGGNA 114
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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: /SIDS1/9cgdata/geneseq/geneseqp-emb
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         747574 segs, 111073796 residues
                                                                   OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDSI/gcgdata/geneseq/geneseqp_embl/AA1998_DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1999_DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000_DAT: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001_DAT:

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Result		Query				
NO.	Score	Match	Match Length DB	DB	ar a	Description
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<u>-</u>	200	-	114	7.7	AAE10807	Xanthomonas ramn
7	111	19.0	344	18	AAWO6600	Time Carronne
~	111	19	344	0	A A 5.7 E O C E	ilyperaelistitve I
•			,	7	COOC / MUN	Pseudomonas sola
4	111	19.0	344	13	AAW62457	Pseudomonas sola
S	111	19.0	344	10	AAW61116	Transmonary
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, ,			# ·	7	WAWO / 04 I	A hypersensitive
_	111	19.0	344	21	AAY71099	Pseudomonas sola
æ	111	19.0	344	21	AAY84860	on this concern of
0	111	9	776	,		avilation of
,	1 ,	70.0	7 7	77	AAEU0/12	Pseudomonas sola
7	111	19.0	385	12	AAR45751	Erwinia amvlovor
11	111	19.0	385	18	AAWO6598	Umpercondition
				ì		ulpersensitive r

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New plant pathogen hypersensitive response elicitor-receptor protein

Erwinia amylovora Erwinia amylovora Hypersensitive res A hypersensitive r Erwinia amylovora A hypersensitive r Erwinia amylovora	Drosophila metanog Drosophila melanog Drosophila melanog Xanthomonas campes Xanthomonas campes A hypersensitive res A hypersensitive r Xanthomonas campes Hypersensitive r	Hypersensitive res Pseudomonas syring A hypersensitive r Drosophila melanog Amino acid sequenc Drosophila melanog Transcription fact Transcription fact Cellular transcrip	
AAW72863 AAW62455 AAW6245114 AAW87639 AAY71093 AAY84854 AAR06710			
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ALIGNMENTS

/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985. /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986. /SIDSI/gcgdata/geneseq/geneseop-embl/AA1987.

'SIDS1/gcgdata,

/SIDS1/gcgdata/geneseg/

/SIDS1

ΩΙ	AAE10807 standard: Protein: 114 AA
XX	
X X	AAE10807;
Į.	18-DEC-2001 (first entry)
X DE	Xanthomonas campestris hypersensitive response ellcitor protein.
Z.	Plant bathoden: hypersensitive resonnes alimitar, upp. strong souletters
KW	disease resistance; Erwinia amylovora hypersensitive resonnes olivitor.
M M	harpin; signal transduction; growth enhancement; insect control;
×	vinciue, impliciue; amilibaccellal.
os	Xanthomonas campestris.
X A	WO200170988-A2.
×	
2 ×	2/-SEP-2001.
ΡĒ	19-MAR-2001; 2001WO-US08728.
×	
PR	23-MAR-2000; 2000US-191649P.
A X	01-DEC-2000; 2000US-250710P.
P.A	(EDEN-) EDEN BIOSCIENCE CORP.
YX PI	Song X. Fan H. Wei 2:
XX	1)
DR	WPI; 2001-590177/66.
ś X	N FOUD; AAULOLZ/.
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understanding the harpin (Erunnia amylovora hypersensitive response elicitor) induced signal transduction pathway in plants. The protein is useful for studying the downstream components of signal transduction pathway in plants which eventually leads to disease resistance, growth enhancement, insect control and stress resistance. Imparting disease resistance to plants through HRE treatment has the potential to treat previously untreatable diseases, treating diseases systemically which might not be treated separately due to cost and avoids the use of infectious agents or environmentally harmful materials. By HRE treatment infectious agents or environmentally harmful materials. By HRE treatment increased quantity of seeds produced, increased percentage of seeds geninated, increased percentage of seeds geninated, increased percentage of seeds geninated, increased percentage of seeds ferminated.
                                                                                                                                                                               receptor in plants for plant pathogen hypersensitive response elicitors (HRE). The plants are made resistant to infection by viruses, bacteria and fungi and are imparted with resistance against environmental stress and insects through HRE treatment. The protein is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ruits, etc. which results in economic benefit to cultivators. Greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              generation from the given plot of plant. The present sequence is
Xanthomonas campestris pv. pelargonii hypersensitive response elicitor
isolated from plants, which upon silencing is used to study plant signal transduction pathways leading to disease resistance and growth enhancement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  increased size and enhanced biomass allow greater revenue
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bacterium; fungus; pathogen; biological control agent.
                                                                                                                                                            to an isolated
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                                                                                                            Disclosure; Page 18-19; 78pp; English.
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                                                                                                                                                       invention relates
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58 saggntgntgnapakdgnanagandpskndpsksqapqsanktgnvddannqdpmqalmq 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- 42 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of hypersensitive response ellcitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the control of insects.
                                                                                                                                                                                                  The elicitor may be used in a new method
                                                                                                                                                                                                           for imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, leaf abrasion, or plant infection with recombinant bacteria (non-infectious to the host plant, e.g. Escherichia coli) expressing the elicitor as a biological control agent, to allow recombinant protein infilitration into the plant. The method confers virus, bacterium or fungus disease-resistance on crops and
                                                                                                                                                                         This sequence represents a hypersensitive response elicitor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas solanacearum hypersensitive response elicitor (HRE)

    with hypersensitive

                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111; DB 18;
Pred. No. 0.00045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 agaggagggvggaggadggsgaggaggangadggn 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.000
17; Mismatches
                                                              Imparting pathogen resistance to plants response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biological control; transgenic plant.
                                                                                                                               Claim 13; Page 50-51; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW75865 standard; Protein; 344 AA.
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25.8%;
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Best Local Similarity 25.8*
Matches 40; Conservative
                                                                                                                                                                                                Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas solanacearum
WPI; 1997-051614/05.
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N-PSDB; AAV54609.
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                                                                                                                                                                                                                                                                                                                                                                     ornamental plants
                        N-PSDB; AAT49316
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                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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Gaps

Length 344; Indels

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polypeptide or protein in a non-infectious form to a plant or plant seed under conditions effective to enhance growth of the plant or plant seed under conditions effective to enhance growth of the plant or plant seed transformed with a DNA molecule encoding a HRE plant seed transformed with a DNA molecule encoding a HRE polypeptide or protein, and growing the transgenic plant or produced from the transgenic seed under conditions effective to produced from the transgenic seed under conditions effective to produce plant growth. HRES (see AAW62454 59) or nucleic acids encoding them (see AAV39972-75) can be used to increase plant growth. The HRES may also result in increased plant height and yield, and effect early germination and maturation of plant seed and early colouration of fruit and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 iledlvklikaalhmqqpggndkgngvggangakgagggggglaealqeleqilaqlgggg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 LLAMFIMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is a hypersensitive elicitor (HRE) protein of Pseudomonas solanacearum. The invention relates to methods of imparting hypersensitive response induced resistance to plants by treatment of seeds. Isolated HRE proteins can be applied to seeds as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathogen resistance; disease resistance; crop protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypersensitive response elicitor; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 111; DB 19;
; Pred. No. 0.00045;
17; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 ------QGGAGMGGGGSVNSSLGGN 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypersensitive response elicitor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 23-24; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW61116 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                   19.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0033230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 Sequence 344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV36430.
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                                   This is the amino acid sequence of a hypersensitive response elicitor (HRE) of Pseudomonas solanacearum. The invention relates to the use of a HRE polypeptide or protein to control insects on plants or plants grown from seed treated with HRE. Also claimed is a method of insect control for plants that involves: (a) providing a transgenic plant or seed transformed with a DNA molecule (see AAV34606-09) encoding a HRE polypeptide or protein (see plants produced from the transgenic plants or transgenic plants produced from the transgenic seeds to control insects. HRE prevents direct insect damage to plants by feeding njury. It kills insect close to plants, and interferes with insect larval feeding on such plants. It also prevents insects from colonising host plants and releasing phytotoxins which result in disease damage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 saggntgntgnapakdgnanagandpskndpsksgapgsanktgnvddanngdpmgalmg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g.increase in plant height or earlier germination seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypersensitive response elicitor; HRE; growth; transgenic plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.0%; Score 111; DB 19; Length 344; 25.8%; Pred. No. 0.00045; Live 17; Mismatches 54; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the deduced amino acid sequence of the hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 ------QGGAGMGGGGGSVNSSLGGN 113
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Best Local Similarity 25.8
Matches 40; Conservative
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N-PSDB; AAV39975.
                                                                                                                                                                                                                                                                                                                                                                                   344 AA;
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WO9832844-A1.

27-JAN-1998; 27-JAN-1997;

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AAW62457;

AAW62457

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                                                                                                                                                                                                                                                                                                                                                                                                              43 LLAMFIMMM-----LOOSOGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a hypersensitive response elicitor protein (also called hairpin protein) that is able to elicit a hypersensitive response in plants. The specification also describes
means of imparting pathogen resistance to plants grown from the seeds. Alternatively, bacteria containing the gene encoding the HRE can be applied to the plant seeds, or transgenic plant seeds containing a DNA molecule encoding an HRE polypeptide or protein are used. HRE polypeptide sequences from Ervinia chrysanthemi, Erwinia amylovora, Pseudomonas syringae, Pseudomonas solanacearum, Xanthomonas campestris pv. glycines and Xanthomonas campestris palargonii (see AAW61113:18) are provided. The methods can impart pathogen resistance without using agents which are harmful to the environment or pathogenic to the plant seed being treated, or to
                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fragments of an Erwinia hypersensitive response elicitor prand related DNA – used to impart disease resistance to plants, increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypersensitive response elicitor protein; hairpin protein; disease resistance; seed quality; insect control; corn borer; Lepidoptera larvae; transgenic plant.
                                                                                                                                                                                                                                                                         Length 344;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                   19.0%; Score 111; DB 19; 25.8%; Pred. No. 0.00045; ive 17; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                          3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- QGGAGMGGGGSVNSSLGGN 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 15-16; 94pp; English.
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                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                 344 AA;
                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                adjacent plants.
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                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW87641;
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application of a hypersensitive response elicitor protein to plants to
                                                                                                                                                                                                                                               58 saggntgntgnapakdgnanagandpskndpsksqapqsanktgnvddanngdpmqalmq 117
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       --00LD0 42
                                                                                                                                                                                                                                                                              43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPONGQOEGLSPLTOMLMOIVMOLMON- 94
            The protein, in non-infectious form, is applied to plants to impart disease resistance (to a wide range of viral, bacterial and fungal pathogens), to improve growth (yield, quantity and quality of seeds, to provide earlier germination etc.) and to control insects (e.g. coborers, Lepidoptera larvae etc.) The same results are provided by transgenic plants expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response elicitor; environmental stress resistance; plant.
m other pathogenic organisms is applied to plants to impar
                                                                                                                                                                                           44;
                                                                                                                                                              Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas solanacearum hypersensitive response elicitor.
                                                                                                                                                                                          Indels
                                                                                                                                                           ; Score 111; DB 20;
; Pred. No. 0.00045;
17; Mismatches 54;
                                                                                                                                                                                                                     3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
hypersensitive response elicitors from other
                                                                                                                                                                                                                                                                                                                                         95 ------QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 26-27; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY71099 standard; Protein; 344
                                                                                                                                                            19.0%;
25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EDEN-) EDEN BIOSCIENCE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US26039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0107243.
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                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    impart stress resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wei Z, Schading RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376566/32,
                                                                                                                                                                          Local Similarity
                                                                                                                 344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD00674
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                                                                                                                                                                                        40;
                                                                                                                   Sequence
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY71099;
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Matches
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Length 344;

DB 21;

Score 111;

19.0%;

Query Match

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Score 111;

19.08;

Query Match

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Hypersensitive response elicitor; oomycete; transgenic plant; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         response to infection of the plant by an oomycete. The chimeric gene is used in gene therapy. The chimeric gene is useful as an effective and safe means of controlling plant-pathogenic fungi, particularly comycetes, which are responsible for major crop loss and is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for producing transgenic plants of the invention. The present sequence is Pseudomonas solanacearum hypersensitive response elicitor protein.
                                                                                                            58 saggntgntgnapakdgnanagandpskndpsksqapqsanktgnvddannqdpmqalmq 117
                                                                                                                                                                                                 118 lledlvkllkaalhmqqpggndkgngvggangakgagggggjaealqeieqilaqlgggg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecule encoding a hypersensitive response elicitor protein or polypeptide, promoter operably linked 5' to the first DNA molecule to induce transcription of the first DNA molecule in response to activation of the promoter by an oomycete and a 3' regulatory region operably linked to the first DNA molecule. The invention also relates to a transgenic plant resistant to disease resulting from comycete infection, the transgenic plant including the chimeric gene, wherein the promoter induces transcription of the first DNA molecule in
                             44; Gaps
                                                                           ---00LDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New chimeric gene, useful for controlling plant-pathogenic fungi and producing oomycete-resistant transgenic plants, comprises first DNA encoding hypersensitive response elicitor, promoter and regulatory
                                                                                                                                                             43 LLAMFIMMM----LLQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas solanacearum hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a chimeric gene that includes a first DNA
                             Indels
; Pred: No. 0.00045; 17; Mismatches 54;
                                                                   3 SIGNNFSNIGNLOTM -----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                  178 agaggagggygaggaggaggaggangadggn 212
                                                                                                                                                                                                                                                           --- QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; crop loss; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 16-17; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Æ
                                                                                                                                                                                                                                                                                                                                                                                                               AAE06712 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORR ) CORNELL RES FOUND INC.
  25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
Best Local Similarity 25.8 Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488791/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bauer DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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AAR45751 RESULT

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GSDANQ -- ECGNEQPQNGQQ ---- EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGGSVNSSL 110
                                                                                                               5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erwinia amylovora, with a mol.wt. of 37,000. The elicitor has a prof. 4.3, thermostability at 100 deg C for at least 10 min, and contains no cysteine. The elicitor may be used in a new method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacteria (non-infectious to the host plant, e.g. Escherichia coll) expressing the elicitor as a biological control agent, to alllow recombinant protein infiltration into the plant. The method confers virus, bacterium or fungus disease-resistance on crops and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a hypersensitive response elicitor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, leaf abrasion, or plant infection with recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Imparting pathogen resistance to plants - with hypersensitive response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypersensitive response; elicitor; Erwinia amylovora; plant; disease-resistance; Escherichia coli; infiltration; virus; bacterium; fungus; pathogen; biological control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.0%; Score 111; DB 18; 31.5%; Pred. No. 0.00052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.0%; Score 111; DB Best Local Similarity 31.5%; Pred. No. 0.00 Matches 39; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 46-47; 69pp; English.
                                                                                                                                                                                                                                                                                                              AAW06598 standard; Protein; 385 AA
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erwinia amylovora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beer SV, Wei Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT49314
                                                                                                                                                                   111 GGNA 114
                                                                                                                                                                                                           236 dqss 239
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                                                                                                                                                                                                                                                                    RESULT 1
AAW06598
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                                                                                              58 saggntgntgnapakdgnanagandpskndpsksgapgsanktgnvddanngdpmgalmg 117
                                                                                                                                                                 Gaps
                                                                 --00LDQ 42
                                                                                                                                          LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HR-elicitor; fire blight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The hrpw gene was isolated from E.amylovora using a 48-fold degenerate oligonucleotide probe corresponding to amino acids 9-15 at the N-terminus of harpin. The 4KD protein encoded by the hrpw gene is a hypersensitive response elicitor protein. The harpin is thought to be an archetype for HR elicitors from phytopathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosaceae; apple; pear; phytopathogenic bacteria; defence reaction; hypersensitive reaction and pathogenicity; hrpN; gene cluster; ds.
                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amylovora - and DNA encoding it, useful for developing harpin
inhibitors to prevent e.g. fire blight of fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypersensitive response elicitor protein derived from Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 385;
                         Indels
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  Pred. No. 0.00045;
; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "corresponds to CAG codon" Misc-difference 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "corresponds to CAC codon"
                                                            SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
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                                                                                                                                                                                                                                                     178 agaggaggaggaggaggaggaggaggangadggn 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laby
                                                                                                                                                                                                                            -- QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harpin; hypersensitive response elicitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  AAR45751 standard; Protein; 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 27-28; 47pp; English.
Best Local Similarity 25.8%; Pr
Matches 40; Conservative 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collmer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0907935.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia amylovora harpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-035054/04.
N-PSDB; AAQ55751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          AAR45751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacteria.
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7;

Gaps

16;

48;

Length 385; Indels a

7;

Gaps

Indels 16;

48;

176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglggggggnagtgl 235

a ŏ Hypersensitive response elicitor; HRE; growth; transgenic plant.

Erwinia amylovora.

W09832844-A1

Erwinia amylovora hypersensitive response elicitor (HRE).

09-NOV-1998 (first entry)

. AAW62455;

AAW62455 standard; Protein; 403 AA.

AAW62455

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This is the amino acid sequence of a 39 kDa, heat stable hypersensitive response elicitor (HRE) of Erwinia amylovora. The invention relates to the use of a HRE polypeptide or protein to control insects on plants or plants grown from seed treated with HRE.

Also claimed is a method of insect control for plants that involves:

(a) providing a transgenic plant or seed transformed with a DNA complecule (see AAV54606-09) encoding a HRE polypeptide or protein (see AAW75862-67); and (b) growing the transgenic plants or transgenic plants produced from the transgenic seeds to control insects. HRE prevents direct insect damage to plants by feeding injury. It kills insects close to plants, and interferes with insect larval feeding on such plants. It also prevents insects from colonising host colons.
176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglgggggggggg1 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the
                                                                                                                                                                                                                                                      Erwinia amylovora hypersensitive response elicitor (HRE).
                                                                                                                                                                                                                                                                                      Hypersensitive response elicitor; HRE; insect resistance;
                                                                                                                                                                                                                                                                                                     biological control; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 9-10; 75pp; English.
                                                                                                                                                             AAW75863 standard; Protein; 403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0039226.
                                                                                                                                                                                                                          07-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-495374/42.
N-PSDB; AAV54607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        control of insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zitter TA;
                                                                                                                                                                                                                                                                                                                                  Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 AA;
                                                                                      236 dgss 239
                                                          111 GGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                               409837752-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-1998.
                                                                                                                                                                                              AAW75863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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(CORR) CORNELL RES FOUND INC.

Wei Z;

Beer SV, Qiu D,

98WO-US01507. 97US-0036048.

27-JAN-1998; 27-JAN-1997;

30-JUL-1998

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enhance plant growth. HREs (see AAW62454.59) or nucleic acids encoding them (see AAV39972-75) can be used to increase plant growth. The HREs may also result in increased plant height and yield, and effect early germination and maturation of plant seed and early colouration of fruit and plants. E. amylovora HRE can be applied to tomato plants to enhance growth without causing disease in that species; this bacterium is a pathogen of apple and pear but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                            response elicitor polypeptide or protein which may also effect, e.g. increase in plant height or earlier germination seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the deduced amino acid sequence of the 39 kDa, heat stable hypersensitive response elicitor (HRE) of Erwinia amylovora. A method of enhancing growth in plants comprises: (a) applying a HRE polypeptide or protein in a non-infectious form to a plant or plants grown from the seed, or (b) providing a transgenic plant or plants grown from the seed, or (b) providing a transgenic plant or polypeptide or protein, and growing the transgenic plant or polypeptide or protein, and growing the transgenic plant or provided from the transgenic seed under conditions effective to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.0%; Score 111; DB 19;
Best Local Similarity 31.5%; Pred. No. 0.00055;
Matches 39; Conservative 21; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 15-16; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-427940/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 AA;
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV39973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of tomato.
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48; Indels 16;

19.0%; Score 111; DB 19; Length 403; 31.5%; Pred. No. 0.00055; tive 21; Mismatches 48; Indels 16

Conservative

Similarity

Query Match Best Local Sim Matches 39;

57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110

5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56

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57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110
            118 gnnttsttnspldgalginstsgnddstsgtdstsdssdpmggllkmfseim--gslfgd 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease resistance; seed quality; insect control; corn borer;
Lepidoptera larvae; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypersensitive response elicitor protein; hairpin protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                         AAW87639 standard; Protein; 403 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORR ) CORNELL RES FOUND INC. (EDEN-) EDEN BIOSCIENCE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beer SV, Laby RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-070210/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erwinia amylovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV83989
                                                                                                                                                                                                                                           236 dgss 239
                                                                                                                                                                                     111 GGNA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW87639;
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176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglggggggagtgl 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Envinia amylovora. It is heat stable at 100 degc for at least 10 min, has a pl of approximately 4.3, and contains substantially no cysteine. The invention relates to methods of imparting the proteins resistance to plants by treatment of seeds. Isolated HRB proteins can be applied to seeds as a means of imparting pathogen resistance to plants grown from the seeds. Alternatively, bacteria containing the gene encoding the HRB can be applied to the plant seeds, or transgenic plant seeds containing a DNA molecule encoding an HRB polypeptide or protein are used. HRB polypeptide sequences from Ervinia chrysanthemi, Ervinia amylovora, Pseudomonas syringae, Pseudomonas solanacearum, Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      campestris pv. glycines and Xanthomonas campestris pelargonii (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           environment or pathogenic to the plant seed being treated, or to adjacent plants. E. amylovora causes disease in apple or pear but not tomato. However, it elicits a hypersensitive response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thus, E. amylovora can be applied to tomato seeds to pathogen resistance without causing diseases in plants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypersensitive response elicitor; transgenic plant; seed
pathogen resistance; disease resistance; crop protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW61113-18) are provided. The methods can impart pathor resistance without using agents which are harmful to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Imparting pathogen resistance to plants – by applying a hypersensitive response elicitor polypeptide to seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypersensitive response elicitor protein (39 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the 39 kDa hypersensitive elicitor (HRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 18-20; 85pp; English.
                                                                                                                                                                                                                                                             AAW61114 standard; Protein; 403 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qiu D, Wei Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-332931/29.
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                                                      111 GGNA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-1996;
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97US-0048109.

Wei Z;

(first entry)

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The present sequence represents a hypersensitive response elicitor protein (also called hairpin protein) that is able to elicit a hypersensitive response in plants. The specification also describes hypersensitive response elicitors from other pathogenic organisms. The protein, in non-infectious form, is applied to plants to impart disease resistance (to a wide range of viral, bacterial and fungal pathogens), to improve growth (yield, quantity and quality of seeds, to provide earlier germination etc.) and to control insects (e.g. corn transgenic plants expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fragments of an Erwinia hypersensitive response elicitor protein and related DNA - used to impart disease resistance to plants, to increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 111; DB 20; 31.5%; Pred. No. 0.00055; tive 21; Mismatches 48;
                                                                                                                Claim 4; Page 10-11; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Indels

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19.0%; Score 111; DB 19; Length 403; 31.5%; Pred. No. 0.00055;

Query Match 19.0%; Score 111; DB Best Local Similarity 31.5%; Pred. No. 0.000 Matches 39; Conservative 21; Mismatches

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176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglggggggnagtgl 235 a

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Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 11, Appl. Sequence 11, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 53, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 3, Appl. Seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15.00-08-891-26.7 Sequence 7, Application US/08891254
Sequence 7, Incomparity 10.00
TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: However V. TOPORESSEE: Nixon, Hargrave, Devans & Doyle STAFE: No OPERATING STAFE: Ploppy disk COUPTER: REDDRAWER: C-DOS/MS-DOS SUSTWARE: Patent In Release #1.0, Version #1.30 PELIANG DATE: 10-014-1997
SEARCH APPLICATION NATA: 10-014-1997
CLASSEPICATION: 514
5-08-951-300-2

5-08-951-300-2

5-08-195-128-2

5-08-195-128-2

5-08-185-428-9

5-08-288-96-117-5

5-08-188-472-19

5-08-288-96-117-5

5-08-188-075-1

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'cogn2_6/ptodata/2/laa/5A_COMB.pep:*

'cogn2_6/ptodata/2/laa/6A_COMB.pep:*

'cogn2_6/ptodata/2/laa/6A_COMB.pep:*

'cogn2_6/ptodata/2/laa/6A_COMB.pep:*

'cogn2_6/ptodata/2/laa/B_CTUS_COMB.pep:*

'cogn2_6/ptodata/2/laa/Pacyfiles1.pep:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Query Match

19.0%; Score 111; DB 1; Length 344;
Bost Local Similarity 25.8%; Pred. No. 77-6-05;
Matches 40; Conservative 17; Mismatches 54; Indels 44;

; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-891-254-7

178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212

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APPLICANT: Zitter, Thomas A.
APPLICANT: ALL FANON-MIN
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE AND HATGRAVE, DEVANS & DOYLE LL
STREET: P. O. Box 1051, Clinton Square
CITY: Rochester
STREET: New York
COUNTRY: Usey York
ZIP: New York
                                                                   RESULT 3
135-09-030-270A-7
: Sequence 7, Application US/09030270A
: Patent No. 5977060
                                    58 SAGGNIGNIGNAPAKDGNANAGANDPSKNDPSKSOAPQSANKIGNVDDANNODPMOALMO 117
                                                                                                     3 SIGNNFSNIGNLOTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                              43 LLAMFINGM-----LOOSOGSDANDECG--NEOPONGQOEGLSPLTOMLMOIVMOLMON- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%; Score 111; DB 2; Length 344; 25.8%; Pred. No. 7.7e-05; tive 17; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADRESSEE: Mixon, Hargrave, Devans 6 Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIF: 14663
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IRA PC compatible
OPERATING SYSTEM: C-COSANS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nel, Ehong-Min
APPLICANT: Nel, Ehong-Min
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: Induced Resistance in Plants
WHOREN OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon, Hargrave, Davans & Doyle
                                                                                                                                                             95 -----QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                               178 AGAGGAGGAGGAGGADGGSGAGGAGGANGADGGN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICATION NUMBER: US/08/819,539
NG DATE: 17-MAR-1997
SIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSIFICATION: 800
R APPLICATION DATA:
PLICATION NUMBER: 08/475,775
                                                                                                                                                                                                                                                                             -e /, Application US/08819539
No. 585924
L INCORNATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLIN ONLE.

VITORING AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTATION NUMBER: 30.
REFERENCE/DOCKET NUMBER:
FELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.8
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (716) 263-16
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-819-539-7
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ZIP: 14603
ZIP: 14603
ZIP: 14603
COMPUTER READABLE FORM:
WEDIGH TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
FILING ONTE:

CLASSIPICATION 514
PRIOR APPLICATION NUMBER: US 60/039,226
APPLICATION NUMBER: US 60/039,226
APPLICATION NUMBER: 38-FEBS 1997
PROFINEY AGENT INFORMATION:
NAME: GOLDMAN, NICHOBEL L.
REGISTRATION NUMBER: 30,727

SEQUENCE CHARACTERISTIC

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58 SAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQAPQSANKTGNVDDANNQDPMQALMQ 117
                                                                                                                                                                                                                                                                                                                                             118 LLEDLVKLLKAALHWQOPGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGG 177
                                                                                                                                                                                                                                                                         43 LLAMFIMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                  3 SIGNNFSNIGNLOTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
Query Match 19.0%; Score 111; DB 2; L. Best Local Similarity 25.8%; Pred. No. 7.7e-05; Marches 46; Conservative 17; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212 💉
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SIGNNFSNIGHLQTM-----GIGPQOHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IQOSQGSDANQECG--NEQPQNGQQEGLSPLTQMIMQIVMQLMQN- 94
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---- OGGAGMGGGGSVNSSLGGN 113

Beer, Steven V.

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COMPESSEES: MATCHES ENGINEERS AND STREET PROPRIETS TO TOTAL STREET PO. BOX 1051, CLINTON Square POYLE LIP PROPRESSES: MATCHES RESPONSES AND SQUARES PORT AND SQ
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118 LLEDLVKLLKAALHMQQQGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.0%; Score 111; DB 4; Length 344;
25.8%; Pred. No. 7.7e-05;
Live 17; Mismatches 54; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SIGNNFSNIGNLQTM-----GIGPQOHEDSSQQSPSAGSE-------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 LLAMFINMM-----LQOSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
PCT-US96.0819-7
SEQUENCE 7. APPLICATION:
APPLICANT: CONTENT RESEARCH INC. Inc.
APPLICANT: CONTENT RESEARCH INC. Inc.
TITLE OF INVENTION: RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon, Harrave, Devans 6 Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
REDILHY TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/USS6/08819
COMPUTER: Lam L. CONTROL DOS OPERATING SISTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212
                                                                                                                           CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,048
FILING DATE: 2-7-2NA-1997
ATOGNET/AGDET INFORMATION:
NAME: Coldman, Michael L.
RECISTRATION NUMBER: 30,73
REFERENCE/OCCKET NUMBER: 19603/1501
                                 SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 25.8%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-013-587-7
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 344 amino ac.
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us-09-829-124-2.rai

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Query Match 19.0%; Score 111; DB 2; Best Local Similarity 31.5%; Pred. No. 8:9e-05;
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ATTORNY FAGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE: protein US-08-891-254-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 19.0%; Score 111; DB 5; Length 344;
Best Local Similarity 25.8%; Pred. No. 7.7e-05;
Matches 40; Conservative 17; Mismatches 54; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SIGNNFSNIGNLOTM-----GIGPQOHEDSSQQSPSAGSE------QQLDQ 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bear, Zhong Hin
APPLICANT: Bear, Steven V
TITLE OF INVENTION: Induced Resistance In Plants
NITHER OF INVENTION: Induced Resistance In Plants
OCRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCES: 9
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CORRESPONDENCES: 0
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CORPUTER: Induced Reader Correspondence Correspondence Correspondence
CORPUTER: Induced CORPUTER: Induced Correspondence
CORPUTER: Induced Correspondence

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PILING DARE: 10-UDL-1997
CLASSIFICATION: 514
OOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quence 3, Application US/08891254 tent.No. 5776889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-08819-7
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5 CHNFSNIGNL---OTHGI-GPOOHEDSSOOSPS-AGSEQOLDOLLAMFINAHLQOS---0 56
1118 GHNTFISTHSEDQAAGHSTSOONDOFTSOSSOPHQOLLAMFELHA--QSLEGD 175
1118 GHNTFISTHSEDQAAGHSTSOONDOFTSOSSOPHQOLLAMFELHA--QSLEGD 175
                                                                                                                                                                                                                                                                                           57 GSDANO--ECGNEOPONGOO----EGLSPLTOMIMOIVMOIMONGGAGMGGGGSVNSSL 110
Query Match 19.0%, Score 111; DB 1; Length 385; Best Local Similarity 31.5%, Pred. No. 8.9e-07. Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wel, ZARANTON: APPLICANT: Wel, Zhong Hin Zhung Kesponse TITLE OF INVENTION: Hapersensitive Response NUMBER OF SEQUENCES: ADDRESSE: ADDRESSE: NIXON: Hagrave, Devans & Doyle STRET: Clinfon Square, P.O. Box 1031
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: NIXON: Hagrave, Devans & Doyle STRET: Clinfon Square, P.O. Box 1031
COUNTRY: U.S.A.
COUNTRY: U.S.A.
MEDIUM TYPE: Flopy disk
COMPUTER: LBM PC Compatible
OPERATING STSTEM: PC-COS/MS-DOS
SOFTWARE: PERCET IN-MR-197
CLASSIPICATION NUMBER: US/08/819,539
FILING DATE: 17-MR-197
CLASSIPICATION NUMBER: 08/475,775
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236 DGSS 239

Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps

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118 GNNTTSTINSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSBIM -- QSLFGD 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Watch 19,0%; Score 111; DB 5; Length 385; Best Local Suinlarity 31.5%; Pred. No. 8.9e-08; Matches 39; Conservative 21; Mismatches 48; Indels
                                                                                                                      Sequence 3, Application PC/TUS9608819
GENERAL INFORMATION:
TITLE OF INVENTION:
TOTAL OF INVENTION:
TITLE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: NOW TOTA

COUNTER: U.S.A.

Z.P: 14603.A.

Z.P: 14604.A.

COMPUTER: READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: TBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/NG-DOS

SOFTAME: PEtentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

RELING DATE:

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19603/10051
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APPLICATION NUBER: US 08/475,775
FLLING DATE: 07-7UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michel L.
REDISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULT. 11
US-08-200-7144-2
Sequence 2, Application US/08200724A
Fatent No. 584968
GRERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bauer, David W.
Beer, Steven V.
Collmer, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wel, Zhong-Win
APPLICANT: Bauer, David W.
APPLICANT: Beer, Steven V.
APPLICANT: Collmer, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein PCT-US96-08819-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (716) 26
INFORMATION FOR SEQ ID
SEQUENCE CHARACTERIS
LENGTH: 385 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
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236 DGSS 239
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                                                        RESULT 10
PCT-US96-08819-3
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Per-0593-06243-2
Sequence To. Application PC/TUS9306243
Sequence To. Application PC/TUS9306243
Sequence To. Application PC/TUS9306243
Sequence To. Application Set. Application Set. Sheng Tang He, and Ron J. Laby.
APPLICANT: Beer, Alan Collmer, Sheng Tang He, and Ron J. Laby.
ITILE OF INVENTATION: Elicitor of the Hypersensitive Response in Plants CORRESSONDERS: Shape Associates
STREET: 25 Stytop Drive
CTTY: Trumbull Stytop Drive
CTTY: Trumbull Associates
STREET: 25 Stytop Drive
COUNTRY: USA
CATE: Connecticut
COUNTRY: Hocitical
COUNTRY: Hacitical
COUN
                                                                                                                                                                    57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGAGAGGGGSVNSSL 110"
                                                        5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.0%; Score 111; DB 5; Length 385; Best Local Similarity 31.5%; pred. No. 8, 9e-07. Matches 39; Conservative 21; Hismatches 48; Indels 1 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRF D-1172
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PRIOR APPLICATION NUMBER: 907,935
FILING DATE: 01-UL-1992
ATORNEY AGENT INFORMATION:
NAME: GOOGG H. TARMAK
RECISENATION NUMBER: 26,824
REPERBUCKOCKET NUMBER: GRF ITELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide
PCT-US93-06243-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linea
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57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.0%; Score 111; DB 2; Length 403; Beat Local Similarity 31:5%, Pred. No. 9,4e-0; A Hatches 39; Conservative 21; Mismatches 48; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELICITOR OF THE HYPERSENSITIVE RESPONSE IN PLANTS
COMPUTER: LBM PC. COMPUTED.
COMPUTER: LBM PC. COMPUTED.
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
FILING DATE: US 90/030,270A
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/039,226
FILING DATE: 28 FEB-199
ATTOREY AREA INFORMATION:
NAME: Coldman, Hicheel L.
RECISTRATION NUMBER: 30,727
REFERENCE/DOCKET HUMBER: 19603/1521
TELECOMMUTATION HUMBER: 19603/1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTR:

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

KEDING TYPE: ROAPO disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: Petentin Release #1.0, Version #1.30

TOWN DATE:

OPERATING SYSTEM:

OPERATING SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BEEF, Steven V.
APPLICANT: Wel, zhong-Min
APPLICANT: Collmer, Alan
APPLICANT: Collmer, Alan
APPLICANT: Leby, Rong-Yang
APPLICANT: Collmical APPLICATION OF THE HYPER
TITLE OF INVENTION: IN PLANTS
CORRESPONDENCES: 5
CORRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 GGNA 114
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US-08-851-376A-2
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Best Local Similarity 31.5%; Pred. No. 9.4e-05;
Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GNNFSNIGNL---OTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
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Patent No. 597/060
Patent No. 597/060
Patent No. 597/060
APPLICANT: Zitter, Thomas A
PPLICANT: Zitter, Thomas A
PPLICANT: Well, Zhong Hin
TITLE OF INVENTION: INSECT CONTROL HITH A
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
NUMBER OF SEQUENCES: 10
ADDRESSEE: NIXON: BASTGAVE, Devans & Doyle LLP
                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
STRET: Clinton Square
CITT: Rochester
CITT: Rochester
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2. 23-724A
2. 23-725E-1994
ION: 530
INFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIOW TYPE: Floppy disk
COMPUTER: 18M PC Compatib
OPERATING SYSTEM: PC-DOS,
SOFTWARE: Patentin Releas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       # MOLECULE TYPE: peptide US-08-200-724A-2
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US-09-030-270A-3
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48; Indels 16;

05-MAY-1997

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57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGNGGGGSVNSSL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLLAMFINMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.0%; Score 111; DB 4; Length 403; Best Local Similarity 31.5%; Pred. No. 9,4e-0; Marches 39; Conservative 21; Wismatches 48; Indels
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APPLICANT: 011, Dewen
APPLICANT: 011, Dewe
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WEDDIN TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PARENTER RELEASE #1.0, Version #1.30
CHRRETT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                      TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-984-207-3
INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1::
236 DGSS 239
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US-09-013-587-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
19.0%; Score 111; DB 4; Length 403;
Best Local Similarity 31.5%; Pred. No. 9.4e-05;
Matches 39; Conservative 21; Mismatches 48; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 14603E PORK:
WEDINH TYPE: Floppy disk
WEDINH TYPE: Floppy disk
COMPUTER: IBM FO COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFRAME: PATENTIN Ratesse #1.0, Version #1.30
APPLICATION NUMBER: US/08/984,207
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STREET: P.O. Box 1031, Clinton Square
CITY: Rechester
STARE: New York
COUNTY: New York
ZIP: 14603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10-3
Sequence 3, Application US/08984207
Sequence 3, Application US/08984207
Sequence 3, Application US/08984207
GREEAL INFORMATION:
APPLICANT: Qut, Deven
APPLICANT: Welt, Zhong-Min
                                                                                                                                                                                                                                                                          TELEFAX: (716) 265-1600
INPORMATION FOR ESO ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 403 maino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-376A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 DGSS 239
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US-09-013-587-3

Ouery Match 19.0%; Score 111; DB 4; Length 403; Best Local Similarity 31.5%; Pred. No. 9.4e-05; Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps

111 GGNA 114

236 DGSS 239

Search completed: June 28, 2002, 10:21:52 Job time: 319 sec

81 13.9 1051 2 151904 81 13.9 1102 2 139943 80 13.7 807 2 A53225	80 13.7 1366 2 B86292 79 13.5 454 2 716429-	79 13.5 648 7 504832 79 13.5 806 2 713690 79 13.5 942 2 702446 79 13.5 1005 2 565149		78 13.4 1018 77 13.2 658		ALIGNMENTS	RESULT 1	Cypecies: Pseudomonas acolanacearum Cypecies: Pseudomonas acolanacearum Cybete: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999 CyAccession: S4107); S38621	EMBO J. 13, 531-553, 1994. EMBO J. 13, 531-553, 1994. A.Tille: PopAl, a protein which induces a hypersensitivity-like response on special A; Reference number: 541707; MUID:94148001 A.Sccession: 541707 A.Sccession: Preliminary	Arroteatus type: DNA Arrotes: 1734 (ARLA) Arcross-references: EMBL:227092; NID:g414909; PIDN:CAAB1615.1; PID:g414910	Query Match 19.0%; Score 111; DB 2; Length 344; Best Local Similarity 25.8%; Pred. No. 0.0016; Matches 40; Conservative 17; Mismatches 54; Indels 44; Gaps 5;	QY 3 SIGNNESNIGNIZOTMGIGPQQHEDSSQQSPSAGSEQQLDQ 42		0y 43 LLAMPINONLOGSGGSDANGECGNEOPQNGGOGGLSPLTQHLMQIYMQLMQN- 94	QY 95QGACMGGGGSVNSSLGGN 113	178 AGAGGAGGCYGGAGGADC	RESULT 2 T08471	harpin - Erwinia amylovora	C;Date: 11-Uun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999 C;Accession: TOB471	Kilaby, K.J.; Kim, J.F.; Beer, S.V. Submitted to the BMED Data Library, March 1999 A. Paferanca sumbon, A. 15.17	A; Accession: Toward Andrews.	A.MOLECULE TYPE: ANALYSIA LEGISLACED ITOM GB/EMBL/DDBJ A.ROSIQUES: 1-403 CLABS	A:Cross-references: EMBL:M92994; NID:g4309677; PID:g4309678 A:Experimental source: strain 321 C:Generios:	V. Generalis A. Generalis
Gencore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	Run on: June 28, 2002, 10:16:58 ; Search time 14.36 Seconds (Without alignments) 762.826 #111ion cell undates/sec	Title: US-09-829-124-2 Perfect score: 584 Sequence: 1 MDSIGNNFSNIGNLQTMGIGOGGAGMGGGGGSVNSSLGGNA 114	Scoring table: BLOSUM62 Gapext 0.5 Gapext 0.5	Searched: 283138 segs, 96089334 residues	Total number of hits satisfying chosen parameters: 283138	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : PIR_71:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	g Query	score Match Length DB	111 19.0 344 2 111 19.0 403 2 96.5 16.5 272 2	4 96.5 16.5 1596 2 A3304 hypothelical prote 5 90.6 16.4 2 086885 hypothelical prote 6 92.5 15.8 3498 2 722330 hypothelical prote 7 72230	90.5 15.5 748 2 H85294 90.5 15.5 748 2 D65795 91 15.1 768 2 D65795	90 15.4 3190 2 128218 89.5 15.3 597 1 337849 88 15 1 2414 2 88.349	87 14.9 728 2 521912 87 14.9 728 2 521912	86 14.7 794 2 710119 85.5 14.6 195 2 G83170	85.5 14.6 521 2 A40252 85.5 14.6 641 2 PC7036	84.5 14.5 915 2 \$24577 84 14.4 447 2 T18447	83 14.2 426 2 T51861	93 14.2 1102 2 JC6316 83 14.2 1655 2 T13998 82.5 14.1 281 2 C04408	82.5 14.1 1145 2 001400 82.5 14.1 1480 2 548440	82 14.0 696 2 81 13.9 660 2

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Pupperhetical protein F2J7 4 [imported] - Arabidopsis thaliana
Cispeties Arabidopsis thaliana (mouse-ear cress)
Cibaces 2001 (Cibace 107-14 [imported] - Arabidopsis thaliana (mouse-ear cress)
Cibaces 2001 (GR358)
Chin Chin Ching (M. K.) Conn, L.; Conway, A.B.; Conway, A.R.; Keul, S.; White, O.; Alor Ching, W. K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.B.; Dewar, Nathbors, B.; Huizar, L.
Nature 408, 816-8202, 2000 (ar.)
Alathbors: Hunter, J.L.; Jenkis, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
C.A.; Li, J.E., Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzi, M.; Mizzo, M.; Rooney, T.; Rooley, D.; Sakano, H.
Alathbors: Satzbarg S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Talli, Rer, M.; Wu, D.; Yu G.; Fraser C.M.; Wu, D.; Yu G.; Fraser C.M.; Wu, D.; Yu G.; Fraser C.M.; Wu G.; Fraser C.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-534 <570>
A.Cross-references: GB:AE005172; NID:g10092326; PIDN:AAG12737.1; GSPDB:GN00141
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R.Mortinore, B. Submitted to the EMBL Data Library, June 1995
A.Reference number: 219549
A.R.Cossion: 72230
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Moclecule type: DNA
A.R.Cossion: 74396
A.R.R.Cossion: 74396
A.R.R.Cossion: 74396
A.R.R.Cossion: 74396
A.R.R.Cossion: 74396
A.R.R.Cossion: 74396
A.Cross-references: EMBL:24988B; PIDN:CAA90064.1; GSPDB:GN00028; CESP:F47A4.2
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C.Species: Caenorhabditis elegans
C.Date: 15-Oct.1999 *sequence_revision 15-Oct-1999 *text_change 18-Feb-2000
C.Accession: 722310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1428 QQQQQQQHMGPGAANNMQMQQLLQQ-----QQSGGG-----GNMAASQMQMTSMH-MT 1474
                                                                                                                                                                                                                                                                                                    Ouery Match 16.5%: Score 96.5; DB 2; Length 1596; Best Local Similarity 28.8%; Pred. No. 0.23; Matches 32; Conservative 7; Hismatches 39; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 ОННООООООООООООООНОІТОІОННН----ООООООАЅРІЛЮМОООТЅРІЛЮМОООТЅРІЛ 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 QQHEDSSQQSPSAGSEQOLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 OCHEDSSQQSPSAGSEQQLDQLLAMFINMNLQQSQGSDANQECGNEQPQNGQQEGLSPLT
A.Cross-references; GB:X54251; NID:g8203; PIDN:CAA38152.1; PID:g8204
A.More: Strain Canton S
C.Genetics: Typase:mer: Typase:mer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1475 QTQQQITMQQQQQFVQSTTTTTHQQQQMQMGPGGGGGGGGGGGGGGANNNNGG 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 534;
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Best Local Similarity 34.1%; Pred. No. 0.077;
Marches 31; Conservative 4; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 QMQQQQQQQQQWVMGGQAFAQAPGRSQQGGGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ypothetical protein - Deinococcus radiodurans (strain R1)
; Species: Delnococcus radiodurans
; Species: Delnococcus radiodurans
; Date: 1999 #sequence_revision 03-Dec-1999 #text_change 31-Nar-2000
; Accession: 07548
; March 1999 #sequence_revision 03-Dec-1999 #text_change 31-Nar-2000
; Milton 0., Elsen, J.A., Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shan, M.; Vamathavan, J.G.; Praser, C.M.
M.; Shan, M.; Venter, J.C.; Fraser, C.M.
; T.J. 1577, 1999
; T.H.La: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
; Reference number: A75250; MUID: 20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sisteus: preliantary
Modacule type: DNA
Residues: 1-272 <HHID:
Ignosa references: GB-AB001882; GB:AE000513; NID:g6457865; PIDN:AAF09792.1; PID:g645787
Tapperlamental source: strain Rl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Titte: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually Reference number: A36391; MUID:91065516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Drosophila melanogaster
Clutter 07-Sep-1990 (sequence_revision 07-Sep-1990 *text_change 21-Jul-2000
C.Nocession: A.6391, A.3106; 51514
Rismoller, D.; Friadel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B.
Genes Dev. 4, 1688-1700, 1990
                                                                                                                                                                                                                                                                        118 GNNTSTTNSPLDQALGINGTSQNDDSTSGTDSTSDSSDPWQQLLKMFSEIM--QSLFGD 175
                                                                                                                                                                                                                                                                                                                                                                    57 GSDANG--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                              176 GODGTQGSSSGGRQPTEGEQNAYRKGVTDALSGLMGHGLSQLLGNGGLGGGGGGRAGTGL 235
                                                                                                                        48; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDSIGNNESNIGNIQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----MLGFQQGQTPDM 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mam protein - fruit fly (Drosophila melanogaster)
s: mastermind protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.5; Score 96.5; DB 2; Length 272;
Best Local Similarity 25.5%; Pred. No. 0.039;
Watches 39; Conservative 15; Mismacches 36; Indels 6
                                  Query Match 19.0%; Score 111; DB 2; Length 403; Best Local Similarity 31.5%, Pred. No. 0.010; Matches 39; Conservative 71; Mismatches 49; Indels Matches 39; Conservative 71; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 LMQNQGG----AGMGG--GGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1596 <SMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 DGSS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Gene: DR0201
A, Map position: 1
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Typothetical protein W06B11.2 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 18-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Accession: T26218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-3190 <AKI>
A; Cross·references: EMBL: U88570; NID:91916939; PID:91916930; PIDN:AAB53050.1
                                                                                                                                                                                                                                                                                                                                                                     572 NAMNNPNSNTGKQE--GFSSQNPTPNSNQSPSSSSQQRHNLVTGGFPNSPQMQQQQRTMN 629
                                                                                                                                                                                                                                                                                                                                                                                                                                               62 QECGNEOPQNGQQE------GLSPLTQMLMQIVMQLMQNQGG------AGMCGGGS-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 GPT-NILPQNHPHQLQSPHSHGNTPEGOMLHQLLQEMSENGGSVQQQQAFSGQSGSNSNA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 YONMANLITSFGAMGLGPQOIQQRDPQMFQQPILHEPIQGMAQNGFGQQOVFFTQMQNQQH 256
                                                                                                                                                                                                                                                                                                          2 DSIGNNFSNIGNLOTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMAMLQQSQGSDAN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oubery Match 15.4%; Score 90; DB 2; Length 707; Bast Local Similarity 26.5%; Pred. No. 0.4; Matches 36; Conservative 7; Mismatches 21; Indels 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 PSAGSEQQLDQLLAMFINMMLQQSQGSDANQECGNEQPQNGQQEGLSPLTQNLMQIVMQL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 27.0%; Pred: No. 0.38; Matches 37; Conservative 18; Mismatches 55; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 205/3; 249/3; 266/1; 337/3; 360/3; 394/2; 425/3; 449/1
A;Note: M7J2.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 POGOAGOOLOOL-----AQOHO-------QOONSQQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-3190 <AKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689 ERNTTASTSNISGGGRA 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 -----VNSSLGGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 | 11 | 1 | 1 | 1 | 1 | 1 | 281 FFGQGPNGMGNGGVMN 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 MONDGGAGMGGGGSVN 107
                                                                                                                                                                                                                                                                                                              δŏ
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Prothetical protein A7492550 [imported] - Arebidopsis thaliana |
| Special Arebidopsis thaliana (mouse-ear cress) |
| Special Arebidopsis thaliana (mouse-ear cress) |
| Stocker | Serber 2001 |
| Serber 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perenn, M.; Barques, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Hohe dumitted to the Protein Sequence Database, April 1998

Reference number: 215452

Accession: 107955

Received type: DAN

Realdules: 1.748 CBEV.

Cross-references: EMBL:AL022197

Experimental source: cultivar Columbia; BAC clone M7J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule Type: DNA,
Mesiduae: 1-14 cspc.
Cross-references: GB:NC_001268; NID:g7269402; PIDN:CAB81362.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 3369 GOOGHQ--PQOSOISQOOQOQQQRRMQAQMQQQQPTAQCQQNRMG--MPSQ-QQSGAAX 3423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thetical protein M7J2.110 - Arabidopsis thaliana ecies: Arabidopsis thaliana (mouse-ear cress) tet: 09-Apr-1999 *sequence_revision 09-Apr-1999 *text_change 13-Aug-1999 cession: n05/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 NAMNNPNSNTGKQE--GPSSQNPTPNSNGSPSSSGQRHNLVTGGFPNSPQMQQQQRTMN 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 QECGNEQPQNGQQE-----AGLSPLTQMLMQIVMQLMQNQGG-----AGMGGGGS-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630 GPT-NILPQNHPHQLQSPHSHGNTPEQQMLHQLLQEMSENGGSVQQQQAFSGQSGSNSNA 688
                                                                                                                                                                                                                                                                                                                                                                              20 GPOQHEDSSQQSPSAGSEQQLDQLLAMFIMMIQQSQGSDANQECGNEQPQNGQGEGLSP 79
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.5%; Score 90.5; DB 2; Length 748;
Best Local Similarity 27.0%; Pred. No. 0.38;
Matches 37; Conservative 18; Mismatches 55; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DSIGNNFSNIGNLOTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDAN 61
                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                   Ouery Match 15.8%; Score 92.5; DB 2; Length 3498; Best Local Similarity 37.6%; Pred. No. 1.3; Matches 32; Conservative 4; Mismatches 42; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3424 SNOMOFOGVRGGOGMG--GMGGSG 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 LTOMLMOIVMOLMONOGGAGMGGGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 -----VNSSLGGNA 114
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689 ERNTTASTSNISGGGRA 705
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A;Gene: AT4g25520
A;Map position: 4
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A.Map position:
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2192 QQQQGAGPGIGPGMANHNQFQQPQGVGYPPQPQQRMQHHMQQMQ-OG--NMGQIGQLPQA 2248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 QQSQGSDANQECG --- NEQPQNGQQEGLSPLTQMLMQIVMQLMQNQGGAGMGGGGGSVNSS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 NLQTMGIG-----PQQHEDSSQQSPSAGSEQQLDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ences: GDB:9862958; OMIM:502700
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Molecule type: protein
Residues: 552-660 <LUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 NSSLGGNA 114
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ferance number: 837832
seasion: 837849
lecule type: DA
Aldes: 1.579 KRES
Assistant 83787
seasion: 83787
ferance number: 827864
lecule type: DA
Assistant 8286C
Itted to the Protein Sequence Database, March 1994
ferance number: 837851
ession: 837853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s type: DNA
s: 1-397 < CUDA:
ferences: EMBL:228032; NID:g486033; PIDN:CAA61867.1; PID:g486034; GSFDB:GN000]
ental source: strain S788C
s: B.; Skalar, J.; van Dyck, L.; Goffeau, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , 125-130, 1994
Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               references: EMBL:X71622, NID:9505182; PIDN:CAB37853.1; PID:94467991
mental sources strain 5288C
3.J.; Rellett, P.J.; Lippard, S.J.
4 to the EMBL Data Library, July 1993
ption: IXRI, a yeast protein that binds to platinated DNA and confers sensitivit
nee number: 839002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. intrastrand crosslink recognition protein - yeast (Saccharomyces cerevisiae)
Alternate names: provient MK1032c; protein YKL245; transcription factor ORD1
Species: Saccharomyces cerevisiaes protein NKL245; transcription factor ORD1
Date: 10-sep-1999 fsequence_revision 10-sep-1999 *text_change 21-Jul-2000
Accession: S78649; S73639; S41668; S39002; AS7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db / 2875 фолскором роспородом ображения предоставления проставления проставления проставления предоставления предоставлен
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15.4%; Score 90; DB 2; Length 3190;
Best Local Similarity 30.1%; Pred. No. 2;
Matches 28; Conservative 6; Hismatches 35; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 GTMGIGPO--OHEDSSQGSPSAGSEQQLDQLLAMFINAMLQOSGGSDANGEGGNEDPONG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2927 QQ ------VNLMQQQQGGPGGPG 2945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 QOEGLSPLTQMLMQIVMQLMQNGGGAGMGGGGS 105
                                                                                            A/Map position: X
C:Superfamily: bromodomain homology
F:1723-1780/Domain: bromodomain homology <BRO>
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: S41668
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C; Genetics:
A; Cross·references: FlyBase: FBgn0015624
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Actual: problainary
Holecule type: mRNA
Hosidues: 1-2414 <CKCA
Cross=references: GB:U01877; NID:9495300; PIDN:AAA18639.1; PID:9495301

Note: In the authors' translation 941-8er is shown after 961 and consequently, res
Indibad, A: N. Kwck, R. P. S.; Laurance, M. E.; Harter, M. L.; Goodman, R. H.

ture 374, 85-88, 1995

Thile: Adeovoriral EIA-associated protein p300 as a functional homologue of the tran
Accession: 560344; MUID:95174889
A;Cross-references: SGD:S0001515; MIPS:FKL032c
A;Map position: 1L
C;Map position: 1L
C;Map position: 1L
C;Map position: 1L
C;Map position: 1MG box homology cHMG1-
F;354-499/Domain: HMG box homology cHMG2-
F;431-499/Domain: HMG box homology cHMG2-
F;431-499/Domain: HMG box homology cHMG2-
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C.Superfamily: unassigned bromodomain proteins; bromodomain homology
C.Feyvords: phosphoprotein: transcription: 2inc finger
19.105-1133-70cmain: bromodomain homology 4800>
F.99.507, 1136,1295,1497,1894,11977, 2052,3320/98inding site: phosphate (Ser) (covalent)
F.1734/Binding site: phosphate (Ser) (covalent) (by protein kinase A) *status predici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXCHET, Y.: Even, N.E.; NewSome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence, J.B.; Lines Dev. 8, 869-884, 1994.

Title: Molecular cloning and functional analysis of the adenovirus ElA-associated Reference number: A5477; WIID:95011587

Accession: A54277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newsome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence, J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 10-Dec-1999
ion: A54277; S60344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 QQQQQQQQAPYQGHFQQSPQQQQQNVYYPLPPQSLTQPTSQSQQQQQQQQQQQANSNSNS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DSIGNNFSNIG---NLQTMGI--GPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DASNSNLLNIGQDHSLQYQGLEHNDSQYRDASHQTP----HQYLMQFQAQPQQQQQQQQ 66
                                                                                                                                                                                                                                                                                                                                                                       Owery Match 15.3%; Score 89.5; DB 1; Length 597; Best Local Similarity 28.1%; Pred. No. 0.38; 25. Indels 19; Matches 36; Conservative 14; Mismatches 59; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omery Match 15.1%; Score 88; DB 2; Length 2414; Best Local Similarity 31.2%; Pred. No. 2.4; Marches 39; Conservative 6; Mismatches 54; Indels 7
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)/Species: Sagittaria sagittifolia (arrowhead)
//Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 GNNFSNIGNLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFINMMLQQSQSDANDEC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 DANOECGNEOPONGO-OEGLSPLTOMIMOIV-----MOIMONGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 D--QETARKLKTSSQEQDGFIRVERGLQIARPSWRESQEWSQSGSGSGYGTGQTGPLP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
14.7%; Score 86; DB 2; Length 794;
Best Local Similarity 29.5%; Pred. No. 1.1;
Matches 36; Conservative 15; Mismatches 53; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 NFSNIGNLQTMGI-----GPQQHEDSSQQSPSA--GSEQQLDQLLAMFIMMLQQSQGS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 GNEOPONGOGEGLSPL----TOMLMOIVMOLMONGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Streams pre-liminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Gross-references: EMBL:M9117; NID:e1008798; PID:e284333
A:X-perimental source: tissue type seed
C:Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.9%; Score 87; DB 2;
Best Local Similarity 28.3%; Pred. No. 0.83;
Matches 32; Conservative 10; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Chen, L.; Fischer, H. submitted to the EMBL Data Library, October 1996 A;Reference number: 217066 A;Accession: F10519
                                                                              A;Gene: FlyBase:br
A;Cross-references: FlyBase:PBqn0000210
C:Superfamily: PoZ domain homology
C;Reywords: zinc finger
F;18-119/Domain: PoZ domain homology <PoZ>
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Job time: 323 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adlecule type: mRNA
Residues: 1-663 - OIB-)
Assidues: 1-229, VV, 231-663 - OIB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                   ol Bello, P.; Whithers, D.; Bayer, C.; Fristrom, J.; Guild, G.; Mittled to the EMBL Data Library, Angust 1990
Pescription: The Drosophila Broad-Complex encodes a family of related, zinc finger-competence number: 821911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accre-TNT1-01-21 protein - fruit fly (Drosophila melanogaster)
- Special Drosophila melanogaster
- Special Drosophila melanogaster
- Accession: S131913, A51356___revision 20-Feb-1995 #text_change 01-Dec-2000
- Accession: S131913, A51356__revision 20-Feb-1995 #text_change 01-Dec-2000
- Special Drosophila Brown C.; Fristrom, J.; Guild, G.
- Dib Bello, P.; Whithers, D.; Bayer, C.; Fristrom, J.; Guild, G.
- Description: The Drosophila Broad-Complex encodes a family of related, zinc finger-con-
- Reference number: S21911
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Dibello, P.R.; Withers D.A.; Bayer, C.A.; Fristrom, J.W.; Guild, G.M.
netics 129, 355-391 1991
Tritle: The Drosophila Broad-Complax encodes a family of related proteins containing 21
Reference number: A53235; MULD:32077389
                                                                                                                                                                                                                                                                                                                                    95 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000 12; D53235
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Wolecule type: mass 222, NV, 231-728 <DI2>
Festaloss: 1-722, NV, 231-728 <DI2>
Note: Sequence extracted from NCBI backbone (NCBIN:79448, NCBIP:79449)
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14.9%; Score 87; DB 2; Length 663;
Best Local Similarity 28.3%; Pred. No. 0.75;
Matches 32; Conservative 10; Mismatches 51; Indels 20;
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                                                                                                                                                                                                                                                           -01-21 protein - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acces: FlyBase:br
Arcos references: FlyBase:FBgn0000210
C:Superfamily: Poz domain homology
C:Keywords: Zinc finger
F:18-119/Domain: Poz domain homology <POz>
11 1
2249 LGAEA 2253
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•	Description	09kw32 xanthomonas					O9w0n3 drosophila	Bringon Carro	Ogetke homo garden	Ogravit detacona	OgyfwB drosophile	OGVENT GLOSOPHILE	Oberes Services	020497 Caenorhahdi	O87264 DS-Indomonas	094486 dirtyostali	065609 arabidopsis
SUMMARIES		;	OT .	Q9KW32	0921J5	O9WXKO	09Y0C9	09RBS0	O9W0P3	O9RBYO	096JK6	09RXV5	09V6W8	09V6W7	09С6М3	020497	087264	094486	065609
		:	g :	7	7	~	'n	ď	'n	~	4	16	'n	'n	10	'n	~	s	70
			march bength bb	139	143	330	838	344	318	339	1173	272	1366	1594	534	3498	424	624	748
	ø	Query	March	32.4	32.4	.19.5	18.9	18.8	18.2	17.9	17.2	16.5	16.5	16.5	16.4	15.8	15.7	15.6	15.5
			2000	189.5	189	114	110.5	110	106	104.5	100.5	96.5	96.5	96.5	96	92.5	91.5	91	90.5
		Result		1		e	4	'n	ω	7	ω	6	10	11	12	13	14	15	16

8 6 8

45 84 14.4 926 5 Q9W3G1 Q9W3g1 drosophila

Page

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58 SAGGNTGNTGNAPAKDGNANAGGANDPSKSQGPQSANKTGNVDDANNQDPMQALMQLLED 117
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NCBI_TaxID=305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNSLATOFG --GSTSNLOVGPSQDTTFGSNQGGNQGISEKQLDQLLCQLISALLQSSKNA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MDSIGNNFSNIGNLQTMGIGPQQHED-SSQQSPSAG-SEQQLDQLLAMFIMAMLQQS--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALM:**ANDO: J. PubMed-10714988;
J.IXINE-20179797; PubMed-10714988;
J. W., MaChanna M.M., White F.F.,
Jentification of two novel hrp-associated genes in the hrp gene
Jates of Xanthomonas oryzas pv. oryzas.";
Batceriol. 18311844-1853(2000).
J. M. ASS1211.1;
JOBENCE 143 AA; 13987 WH; 053EC694CA24IESC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas oryzae pv. oryzae.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burkholderia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.4%; Score 189; DB 2; Length 143; Best Local Smilarity 41.0%; Pred. No. 4.1a-17. Watches 59; Conservative 11; Mismatches 49; Indels 1 Watches 50; Conservative 11; Mismatches 49; Indels 1
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19.5%; Score 114; DB 2; Length 330;
Best Local Similarity 28.4%; Pred. No. 0.0018;
Matches 40; Conservative 15; Mismatches 56; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hikichi Y. 'Ikegami M., Okuno T.;
PopAl OR of Ralsconia Rolameerum.';
Submitted (ARP-1999) to the RBL/GenBank/DDBJ databases.
EMBL, AB026629: BAN77370.11. EMBL/GenBank/DDBJ Gatabases.
SEQUENCE 330 AA. 31997 WH; BEC4CD9E319D4A5 CRC64;
                                                                                                                                                                            0921J5 PRELIMINARY, PRT; 143 AA. 0921J5; 041-147-1999 (TERGLEA). 10, Created) 01-MAY-1999 (TERGLEA). 10, Last sequence update) 01-DBC-2001 (TERGLEA). 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9WXKO PRELIMINARY; PRT; 330 AA.
O9WXKO 01 CONTROL 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
POPAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas.
NCBI_TaxID=64187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-8107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ralstonia.
NCBI_TaxID-305;
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099WXKO
AC 099
AC 090
DT 011
DT 011
DT 010
DT 000
BE PO 000
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56; Indels 30; Gaps

3 SIGNNFSNIGNL QTMGIGPQQH -----EDSSQGSPSAGSEQQLDQ 42

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545 NSSNNSNSSNNNMKSSGFQPQQSQQQQQQT-----QQTQQ------TQQQAQQAP 588
                                                                                                                                     118 LVKLLKAALHMOOPGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGAAGAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 QECGNEQPQNGQQEGLSPLTQMLMQIVMQLMQNQ-----GGAGMGGGGSV----NSS 109
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43 LLAMF-IMMALQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQNQ---- 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sporence PROM N.A.
MEDLINE-9940279; Pubmed-10473630;
MEDLINE-9940279; Pubmed-10473630;
A novel Ras-interacting procein required for chemotaxis and cyclic adenosine monophosphate signal relay in Dictyostellum.*;
MOL. BIOL. Cell 10.12829-3485(1999).
SEMUL: ARISO241; AAA43657.1; -...
SEQUENCE 838 AA; 94059 MW; EAAD911294226808 CRC64;
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(Cteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostellum discoldeum (Slime mold).
Enkaryota; Myestoxoa; Dictyostellida; Dictyostellum.
Mani_TaxiD-44689;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RAS INTERACTING PROTEIN RIPA.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                          178 GAGGGSGAGGAGGANGADGGN 198
                                                                                                                                                                                                                                                        96 --- GGAGMGGGGSVNSSLGGN 113
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Best Local Similarity 31.2
Matches 39; Conservative
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REC STRAIN-BERKELEY;
RA Admar M. D., Celniker S.E., Holf R.A., Evens C.A., Gocoyne J.D.,
RA Admar M.D., Celniker S.E., Holf R.A., Evens C.A., Gocoyne J.D.,
Amanatides P.G., Scherer S.E., Hichred S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortnam J.R., Yandell N.D., Zhang O., Chen L.Z.,
RA Station G.G., Wortnam J.R., Yandell N.D., Zhang O., Chen L.Z.,
RA Station G.G., Wortnam J.R., Yandell N.D., Zhang O., Chen L.Z.,
RA Brandon R.C., Rogers Y. H.C., Elbazel R.G., Champe M., Petiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Landrews Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxedala D., Bortskrogil, E. Baldwin D.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Dobishov S.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Dobishov S.,
Ra Burtis R.C., Busam D.A., Butler H., Cadleu E., Doba I., Distabov S.,
Ra Burtis R.C., Busam D.A., Butler H., Cadleu E., Doba I., Distabov S.,
Ra Burtis R.C., Busam D.A., Butler H., Cadleu E., Doba I., Distabov S.,
Ra Godon K., Doup L.E., Downes M., Dupan-Footh S., Duntov B.C.,
RA Cong F. Gorrell J. H. F., Hernander J.R., Flow I., Distabov S.,
RA Godon K., Doup L.E., Downes M., Dupan-Footh S., Pubroy B.,
R. Godon K., Doup L.E., Downes M., Dupan-Footh S., Duntov B.,
R. Godon K., Doup L.E., Morten G.B., Gelbart M., Glasser K.,
R. Harris N.L., Harvey D., Helman T.J., Hernander J.R., Houva M.,
R. Harris N.L., Harvey D., Kafter C., Kravitz S., Kull D., Lai Z.,
R. Lasko P., Lei Y., Leviteky A.A., Li J., Li Z., Linny Y., Lin X.,
R. Hashon D., Rolling N., Mobarry C., Morris J., Moshrefi A.,
R. Ralson D.M., Pittamn G.S., Pen S., Pollard J., Ward D.,
R. Ralson D.M., Pittamn G.S., Pen S., Pollard J., Ward D.,
R. Ralson D.M., Ralson R.A., Window Y., Welssenber D.R.,
R. Relson D.M., Ralson R.A., Window Y., Welssenber D., Strong R., Snich H.O.,
R. Ralson D.M., Welssen D.R., Weng R.M., Weng S., Kan G., Shon H.,
R. Land G.M., Welssen D.M., Welssen D.R., Shon H.,
R. Land G.M., Welssen D.R., Welssen D.R., Welssen D.R., Shon H.,
R. Land G.M., Welssen D.R., Welssen D.R., Welssen D.R.
                                                                                     Ducsophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidas; Drosophilidae; Drosophila.
                                                                                                                                                                                                          43 LLAMFIMM -----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
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990093, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990094, 990044, 990094, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 9900444, 990044, 990044, 990044, 990044, 990044, 990044, 990044, 990
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PUDMed-1472716;
Gough C.L., Genin S., Zischek C., Boucher C.A.;
Purp genes of Pseudomonas solanacearum are homologous to pathogenicity determinants of animal parthogenicbacteria and are conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-411000;
WEDLING-93307711; PubMed-8116111;
Gough C.L., Genin S., Lopes V., Boucher C.A.,
Homolocy Derween the HPO protein of Pseudomonas solanacearum and
Abscretain proteins implicatedin a signal peptide-independent secretion
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WEDLINE-9444749; PubMed-8190064;
Genin S., Boucher C.A.;
"A superfamily of proteins involved in different secretion pathways in gram, negative bacteria: modularstructure and specificity of N-terminal
                                                                                                                                                                     PARALTME-951-9000;
Van Gijsegem F., Gough C.L., Zischek C., Genin S., Niqueux E.,
Van Gijsegem F., Gough C.L., Zischek C., Genin S., Niqueux E.,
Allat M., Barberis P., German S., Castello P., Boucher C.A.,
"The hrp gene locus of Pseudomonas solanacearum which controls a type
III secretion system, encodes eightproteins related to components of
Mol. Microbiol. 15:1095-1114(1995)."
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MEDLINE-94148001; PubMed-8313899;
MEDLINE-94148001; PubMed-8313899;
*TopAl, a protein which induces a hypersensitivity-like response on specific Petunia genotypes, is secretedvia the Hrp pathway of EMEDO 3. 13:543-553(1994).
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Best Local Similarity 25.8%; Pred. No. 0.0005;
Matches 40; Conservative 16; Mismatches 55; Indels 44;
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MEDLINE-93125128; Pubked-1479894;
Genin S., Gough C.L., Zischek C., Boucher C.A.;
Evidence that the hrpB gene encodes a positive regulator of parhogenicity genes from Pseudomonas solanacearum.";
Microbiol. 6:3065-3076(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96347139; PubMed-8736546; Bogdanove A.J., Beer S.V., Bonas U., Boucher C.A., Collmer A. Coplin D.L., Cornells G.R., Huang H.C., Hurcheson S.W., Panopoulos N.J., Van Gijsegem F.; Unified nomemclature for broadly conserved hrp genes of
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Wol. Genet. 243:112-118(1994),
EMBL; AA243811; CAB58262-11; -.
SEQUENCE 344 AA; 33152 MW; 42A7C5A0C32B0907 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogenic bacteria.";
Plant Microbe Interact. 5:384-389(1992).
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Mol. Microbiol, 36:261-277(2000).
[2]
SEQUENCE FROM N.A.
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Mol. Microbiol, 20:681-683(1996).
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FROM N.A. Stapleton M., Brokstein P., Hong L., Agbayani A., Carison J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.

Gaps

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58 ---GGPGSMQMNPQGPGGPGGLMPGMSPQHQMQQQQQQQMNVPQQGVGVGVGMGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                  54 QSQGSDANQECGNEQP--QNGQQEGLSPLTQMLMQIVMQLMQNQ----------- 96
                                                                                                                                                                                                                                                                                                                           5 GNNFSNIG-----NLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQ 53
, Miranda A., Mungall C.J., S., Phouanenavong S., Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hikich Y., Kanda A., Hasegawa H., Okuno T.;
"popA in Ralstonia solanacearum OE1-1 pathogenic to tobacco.";
Submitteed (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: A803747; BAR84679.1;
SEQUENCE 339 AA; 32807 WW; 613A51A065D3EDC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POPA-OR.
Burkholderia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria: beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                        Length 318;
                                                                                                                                                                                                                                                                                                                                                                         5 GONDGNOGPSSGGGGGGPNNMPMGGFGNQHGNNQQMHMSPQHQQQQQQMGMM
                                                                                                                                                                                                                              Query Match 18.2%; Score 106; DB 5; Length 318 Best Local Stailarity 28.5%; Pred. No. 0.0013. Matches 46; Indels Matches 46; Indels
GODZALEZ M. GURTIN H. LI P., Liao G., Miranda A., Mung
Nunco J., Pacible J., Paragas V., Park S., Phousnenavong
Tu C., Lewis S.E., Rubin G.M., Celnikes S.,
Submitted (GCT-2001) to the EMEL/GenBank/DDBJ databases.
EMEL, AROGISCI, AAL7400.1; -
EMEL, AYOGISCI, AAL7401.1; -
Flybase; PSH00053149; CGT7183
SEQUENCE 318 AA, 35301 MW; EBD4E59A002E5DF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TEE/BLrel. 13, Created)
01-MAY-2000 (TEE/BLrel. 13, Last sequence update)
01-MAY-2000 (TEE/BLrel. 13, Last annotation update)
POPA-OB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 GAGMGGGGSV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 GVGMGGGGVV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia.
NCBI_TaxID-305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9RBYO
O9RBYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q9RBY0
ID Q91
AC Q91
   $ $ $ $ $ $ $ $ $ $ $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
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Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.; *Prediction of the coding agenences of unidentified human genes. XX. *The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro."; NAN Res. 8:8-55(2001).

MEDLINE-21245130; PubMed-11347906;

SEQUENCE FROM N.A.

EMBL, SBOS8722; BAB47448.1; -. NON_TER SEQUENCE 1173 AA; 126815 MW; B3E52EDFE7EEE3BO CRC64;

Homo sapiens (Human). Exkaryota: Metazoa; Chordata: Craniata; Vertebrata; Enteleostoml; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. NCB_Caxi0+9606;

Last annotation update)

101 (TrEMBLrel. 19, PROTEIN (FRAGMENT).

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                                                                                                                                             56 SAGGNIGNIGNAPAKDGNANAGANDPSKNDPSKSQGPQSANKIGNVDDANNQDPMQALMQ 115
                                                                                                                                                                                                                                             116 ILEDLVKILKAALHMOOPGGNDKGNGVGGANGAKGAGGGGLAEALQEIEQILAQPGGGA 175
Query Match
17.9% Score 104.5; DB 2; Length 339;
Best Local Similarity 25.7% Pred. No. 0.002;
Matches 39; Conservative 17; Mismatches 55; Indels 41; Gaps
                                                                                            3 SIGNNFSNIGNLOTM -----GIGPQQHEDSSQQSPSAGSE------00LDQ 42
                                                                                                                                                                                               43 LLAMFINDM-----LOQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQ---- 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    096JK6 PRELIMINARY; PRT; 1173 AA. 096JK6 010 (TEMBLEL: 19, Created) 01-DEC-2001 (TEMBLEL: 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                176 AGAGGAGGGVGGAGGSGAGGANGADGGN 207
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
096JK6
ID 096JK6
AC 096JK6
DT 01-DEC
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Indels 13; Gaps
                                                                                                               22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MDSIGNNFSNIGNLQTWGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20036895; PubMed-10567265; Hickey E.K., Peterson J.D., MAIdelberg J.F., Hickey E.K., Peterson J.D., Obdson R.J., Maid D.H., Nelson W.C., Richardson D.L., Moffer K.S., Oln Haft D.H., Call D. Pamphile W., Crosby W., Shen M., Moffer R.S., Oln Har, P., McDonald L., Otterback T., Zalberski C., Makarova K.S., Arathd L., Dally M.J., Mincon K.M., Fleischmann R.D., McRechum K.A., Nelson K.E., Salaberg S., Smith H.O., Venet J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deinococcus radiodurans
Bacteris, Thermus/Deinococcus group; Deinococcales; Deinococcus,
VIBL_TaxID-1299;
Ouery Match
17.2%; Score 100.5; DB 4; Length 1173;
Best Local Similarity 30.1%; Pred. No. 0.02;
Matches 28; Conservative 12; Mismatches 40; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.5%; Score 96.5; DB 16; Length 272; Best Local Similarity 25.5%; Pered No. 0.012; Matches 39; Conservative 15; Mismatches 36; Indels 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ome sequence of the radioresistant bacterium Deinococcus odurans 81 ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 272 AA; 26985 MW; 18D37805BE73AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NAY-2000 (TrEMBLrel. 13, Created)
MANY-2000 (TREMBLrel. 13, Last sequence update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
HYPOTHETICAL 27,0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 272 AA
                                                                                                                                                                                                                                      82 QML-----MOIVMQLMQNQGGAGMG 101
                                                                                                                                                                                                                                                                             Science 286:1571-1577(1999).
EMBL: AE001882; AAF09792.1; -.
TIGR; DR0201; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9RXV5
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39; Indels 33; Gaps

7; Mismatches

Matches 32; Conservative

1 09:28:20 2002

Mon Jul

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909689 PRELIMINARY; PRT; 1366 AA.
09V688 01-MAY-2000 (TEMBLEAL. 13, Created)
01-MAY-2000 (TEMBLEAL. 13, Last sequence update)
01-MAY-2010 (TEMBLEAL. 16, Last annotation update)
01-MAY-2010 (TEMBLEAL. 16, Last annotation update)
MAM OR CG8118.
MAM OR CG8118.
Prosophila melanogaster (Fruit fly).
Everyotes Medexos. Arthropoda; Trachesta; Hexapoda; Insecta;
Preryotes Neoprexa; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides; Drosophilidae; Drosophila.
91 LMONOGG------AGMGG--GGSVNSSLGG 112
                                                    139 MGGNMGGQSGGGMSLPGGMGGGLGGGLGSILGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i3; mam.
: 141456 MW;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BERKELEY;
MEDLINE-20196006;
                                                                                   RESULT 10
09V6W8
1D 09V6W8
AC 09V6W8;
DT 01-MAY
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RA Addms W D., Celnighter S.E., toll R.A., Evans C.A., Gocoyne J.D.,
RA Adms W D., Celnighter S.E., toll R.A., Evans C.A., Gocoyne J.D.,
RA Genotic R.A., Levis S.E., Holl R.A., Evans C.A., Golle R.P.,
Recorge R.A., Levis S.E., Holl R.D., Zhang O., Chen L.X.,
RA Sutton G.C., Mortman J.R. Historian Else, Tollang O., Chen L.X.,
RA Bandon R.C., Rogers Y. H.C., Blazel R.G., Chempe W., Petiffer B.D.,
RA Man K.H., Dayle C., Baxter E.G., Hell G., Nelson C.R., Miklos G.L.G.,
RA Ballow R.W., Basun A., Baxendale J., Bayraktaroglu L., Basaley E.M.,
RA Ballow R.M., Basun D.A., Berman B.P., Bhandari D., Bolshakov S.,
RA Ballow R., Bennan B.P., Bhandari D., Bolshakov S.,
Rockova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,
RA Berlos B. Delcher A., Deng Z., Mayzaktaroglu L., Basaley E.M.,
RA Cherry J.M., Cavley S., Dahlke C., Daveport L.B., Davies P.
RA Cherry J.M., Cavley S., Dahlke C., Daveport L.B., Davies P.
RA Cherry J.M., Cavley S., Dahlke C., Daveport L.B., Davies P.
RA Doublon R., Doup L.E., Downes M., Dugan-Roche S., Pleischmann W.,
RA Goder K., Obory E.E., Downes M., Dugan-Roche S., Pleischmann R.,
RA Goder K., Gong F. W., Garratz C., Rerriez S., Roukov B.,
RA Ralush F., Karlen G. H., Ke Z., Kenlson J.A., Ketchum K.A.,
RA Rasko P., Let Y., Levitek A.A., Li J., Li Z., Liang Y., Lin X.,
A. Liu X., Mattei B., Murphy B., Murphy L., Mursy D.M., Nalson D.L.,
RA Ralust K., Reallopton K., Stone H., Nalson D.L.,
RA Reliert K., Reallopton K., Stone H., Rash R., Nalson D.L.,
RA Reliert K., Reallopton K., Stone H., Wang X.,
RA Reliert K., Reallopton K., Stone H., Wang X.,
RA Reliert K., Reallopton M., Strong R., Sun E.,
RA Rane E., Spradling A.C., Stebeler F., Shen H.,
RA Rhone E., Spradling A.C., Stebeler F., Shen H.,
RA Rhone E., Spradling A.C., Stebeler F., Shen H., Wang X.,
RA Rhone E., Spradling A.C., Stebeler F., Shen H., Wang X.,
RA Rhone E., Spradling A.C., Stebeler F., Shen H.,
RA Rhone E., Spradling A.C., Stebeler F., Shen H.,
RA Rhone E., Spradling A.C., Stebeler R., Rhon R., Rhon R., Rhon R., Rhon R., Rhon 
                                                                                                                                                                                                                                                                                                DD 1198 GOQQQQHMGPGAANNMQMQQLLQO-----QQSGGG------GNMMASQMQMTSMH-WT 1244
22 QOHEDSSQQSPSAGSEQQLDQLLAMFIMMALQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                     DD 1245 QTQQQITWQQQQEVQSTTTTHQQQQMMQMGPGGGGGGGGGGGGANNNNGG 1295
                                                                                                                                82 OMIMOIVMOLMON---------OGGAGMGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; mam.
; 167263 MW; D4236DA26F70D092 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Let E., Wans, Let G.M., Welsser K.C., Wu D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn000264
SEQUENCE 1594 AA;
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16.5%; Score 96.5; DB 5; Length 1366; 28.8%; Pred. No. 0.073;

Ouery Match Best Local Similarity

us-09-829-124-2.rspt

09C6M3 RESULT 12 09C6M3 ID 09C6M3 AC 09C6M3

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01-DEC-2001 (TrEMBLrel. 19, Last annotation update) F47A4.2 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3424 SNQMQFQGVRQGQQGMG--GMGGSG 3446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                           Canorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                              1426 QQQQQQHKGPGAANNQHQQLLQQ-----QQSGGG-----GNPMASQHQMTSMH-MT 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Araldopele thallana (Mouse-ear cress).

Enkaryota, Viidiphandes (Isteptophyta, Embryophyta, Tracheophyta,
Enkaryota, Mistoliophyta, endicocyledons, core eudicots, Rosidae,
euroalda II: Brasicales; Erassicaceee; Arabidopsis.
Best Local Similarity 28.8%; Pred. No. 0.086;
Matches 32; Conservative 7; Mismatches 39; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436 ОННООООООООООООНОІТОІДНИН----ООООООА БРІМОМОООТ БРІМ 491
                                                                                                                                     22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMALQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                1473 QTQQQITMQQQQQFVQSTTTTTHQQQQMMQMGGGGGGGGGGGGGGGGGGTATTTTAGGQQMMQMGPGGGGGGGGGGGGGGGGAANNNNGG 1523
                                                                                                                                                                                                                                                                                                                                    B2 ONLMOIVMOLMON--------OGGAGMGGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oubry Match 16.4%; Score 96; DB 10; Length 534; BBst Local Similarity 34.1%; Pred. No. 0.028; Matches 31; Conservative 4; Mismatches 44; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408 816-820(2000).

**Erbi. A0079281, AAG50810.1; -.

**Erbi. A0079281, AAG50810.1; -.

**SEQUENCE 534 AA, 57273 HW; 7498816724021101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 57.3 KOA PROTEIN.
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020497,
01-WOY-1996 (TERGELE). 01, Created)
01-JUN-1998 (TERGELE). 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 ONLMOIVMOLM ----- ONDGGAGMGGGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 QNOQQOQDQQNVMGGQAFAQAPGRSQQGGGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAIN-CV. COLUMBIA;
EDLINE-21016719; PubMed-11130712;
heologis A., Ecker J.R., Palm C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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RESULT 13 020497 ID 020497 AC 020497, DT 01-NOV-DT 01-JUN

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3369 GOOGHO--POOSOISOCOCOCOOOXRINGAAQMOCOPTAGGOONRMG--MPSQ-QCSCAAY 3423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 GPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSP 79
oda; Chromadorea; Rhabditida; Rhabditoidea; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-20243785; PubMed-10781092;
Alfano J.R., Charkowish A.O., Deng W.L., Badel J.L.,
Pertickt-Covelaja T., van Dijk K., Collmer A.;
The Pesudomonas syringee HEP pathogenicity island has a tripartite
mosalc structure composed of a cluster of type III secretion genes
bounded by exchangeable effector and conserved effector loci that
contribute to parasitic filtness and pathogenicity in plants.';
Proc. Natl. Acad. Sci. U.S.A. 97.4855-486[1200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.64; Pred, No. 0.58; DB 5; Length 3498;
Best Local Similarity 37.64; Pred, No. 0.58;
Makches 32; Conservative 4; Mismatches 42; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DC3000;
MEDLINE-98422476; Pubwed-9748456;
Charkowski A.O., Alfano J.R., Preston G., Yuan J., He S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C.elegans: A platform for threetigating biology.", carecace 282:2012-2018(1998). EMBL, %49888; CAA90064.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: Z49888: CAA900641.7.
INGERTO: JRR000545: ESF-11.Ke.
INGERTO: PR000054: ESF-11.Ke.
PROSITE: PS00012: ESF-11.UNKNOWN.1.
SEQUENCE: 3498 AA; 400777 WH; 283FFC65A6B9E336 CRC64;
                                                                                                                                                                                 Adrimore B J.; submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Ouery Match 15.7%; Score 91.5; DB 2; Length 424; Best Local Similarity 27.8%; Pred. No. 0.068; Matches 27; Conservative 16; Mismatches 27; Indels 27; Gaps
                                                                                                                                                                            26 DSSQOSPSAG----SEQQLDQLLAMFIMMLQQSQGSDANQECGNEQPQNCQQEGLSPL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.6%; Score 91; DB 5; Length 624;
Best Local Similarity 28.1%; Pred. No. 0.12;
Matches 27; Conservative 10; Mismatches 37; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 QQHEDSSQQSPSAGSEQQLDQLLAMFINAMILQQSQGSDANQECGNEQPQNGQQ---- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF005221; AAC62526.1; -.
EMBL; AF232004; AAF71503.1; -.
SEQUENCE 424 AA; 42910 MM; 7AF4ED059BF79D2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                     01.FEB-1997 (TIEMBLIA. 02, Created)
01.FEB-1997 (TIEMBLIA. 02, Last sequence update)
01.FEB-1997 (TIEMBLIA. 02, Last annotation update)
0RF DG1040 (FRAGNERY).
0RF DG1040 (FRAGNERY).
Dictyostellum discoldeum (Slime mold).
EUNARYORIS MYGETOZOZO DICTYOSTELLIIda, DICTYOSTELlum.
NOBI_TAXID-44689;
                                                                                                                                                                                                                 PRT; 624 AA.
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Search completed: June 28, 2002, 10:23:23 Job time: 150 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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June 28, 2002, 10:19:58; Search time 12.31 Seconds (without alignments)
358.573 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-829-124-2 584 1 MDSIGNNFSNIGNLOTMGIG........QGGAGMGGGGSVNSSLGGNA 114

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		*			SUMMARIES			
 	Score	Match	Match Length	80	CI	D	Description	tion
~	111	19	403	7	HRPN_ERWAM	00	00100	erwinia amv
7	110	18	344	-	POPA_RALSO		09rbs0	•
m	96.5	16.5	1596	Н	MAM_DROME	20	P21519	drosonhila
4	89.5	15	597	Н	IXR1_YEAST	. A.	P33417	saccharomyc
'n	88	15.	2414	٦	P300_HUMAN	00	9472	homo sanien
٥	œ		727	П	BRC1_DROME	10	001295	drosophila
7	86.5	14.8	519	_	ELAV_DROVI	P2	P23241	drosophila
ω (82	14.6	675	-	ECR_AEDAE	Ρđ	P49880	aedes aegyp
ۍ .	8	14.2	353	-	TF2D_DROME	P2	P20227	drosophila
2;	82.5	14.1	1480	-	PAN1_YEAST	P3	P32521	saccharomyc
7;	81	13.9	099	-	GLT3_WHEAT	PO	P08488	triticum ae
77	6 6	13.5	416	-	R23B_MOUSE	P5	P54728	mus musculu
ς;	6/	13.5	648	-	GLT0_WHEAT	P1	P10387	triticum ae
+ -	ر»/ د.هر	13.4	512	 1	FUS_BOVIN	02	8009	bos taurus
2,5	78	13.4	255	Η.	LP61_EIMTE	P1	P15714	eimeria ten
9 1	2 [13.4	1018	٠,	YKZ6_CAEEL	P3	P34333	caenorhabdi
1 5	7	13.2	685	٠,	YYCA_BACSU	P3	P37483	bacillus su
ρ τ	(0.07	13.1	405	н,	YCC8_YEAST	. P2	P25367	saccharomyc
,	0.0	13.	829	٠,	E74A_DROME	P2	0105	drosophila
2 5	76.5		883	٦,	E74B_DROME	P1	P11536	drosophila
77	9/2	13.0	834	٦,	5HTA_DROME	P2	8285	drosophila
77	ני נ		363	٦,	TOB1_MOUSE	90	1471	mus musculu
570	_	12.8	526	н,	FUS_HUMAN	P3	P35637	homo sapien
* 0	0.4.0	12.8	463	٠,	K10_DROME	P1	-	drosophila
0,0	V. 4.		648	-	KAPC_DICDI	P3		dictyosteli
97	V. 4.	12.8	1516	Η.	NCO2_XENLA	60	09w705	xenopus lae
7 6	74.5	12.8	1845	-	ZZ36_HUMAN	60	u136	homo sapien
9 6	۲,	12.7	409		R23B_HUMAN	. P5	P54727	homo sapien
7 (73.5		738	Η.	YKF4_YEAST	P3	•	saccharomyc
2 .	, r	12.6	1043	Η,	FTF1_DROME	P3	_	drosophila
7,0	٠, ږ	12.6	2038	Η,	FSH_DROME	P1	_	drosophila
2 6	73	12.5	569	-	BDNF_XIPMA	8	ς	xiphophorus
33		12.5	593	-	K1CJ_HUMAN	P1		homo sapien

P18480 saccharomyc	004047 Arcsophila P70605 rattus norv P0213 drocabila	P34291 caenorhabd1 P32505 saccharomyc	P03210 epstein-bar P08106 gallus gall	UVZLEY CINCECLIUS 019132 oryctolagus P04730 triticum ae
SNF5_YEAST FUS MOUSE	NONA_DROME KCN3_RAT HMAN_DROME	YKO3_CAEEL	YRR2_EBV HS70_CHICK	GDB3_WHEAT
		7		
905	700 732 378	401 525	634	1435 244
12.5	12.4	12.3	12.3	12.3
73	72.5	72	27.25	72
34 35	36 37 38	39 40	444	444

ALIGNMENTS

	ALIGNMENTS
RESULT HRPN_E ID H	HRPSULT 1 HRPN_ERWAM HID HRPN_ERWAM STANDARD; PRT; 403 AA.
68888	01-APR-1993 (Rel. 25, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 40-MAY-2000 (Rel. 39, Last annotation update) 41-41-41-41-41-41-41-41-41-41-41-41-41-4
80 00	
88	Erwinia. NCBI_TaxID=552;
R R R	[1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-15. STRAIN=EA321;
R'A	MEDLINE-92320301; PubMed-1621099; Wei ZM., Laby R.J., Zumoff C.H., Bauer D.W., He S.Y., Collmer A.,
RA RT	Beer S.V.; "Harpin, elicitor of the hypersensitive response produced by the
RT RL	hogen Erwinia amylovora."; :57:85-88(1992).
R G	[2] REVISTONS
. S.	STRIN-EA321;
¥ ¥	Laby K.J., Kim J.F., Beer S.V.; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
ပ္ပင္	-!- FUNCTION: ELICITS THE HYPERSENSITIVE RESPONSE (HR) IN THE PLANT
88	REQUIRED FOR PATHOGENICITY IN HOST PLANTS.
ខ្លួ	-!- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.
ខ្លួ	This SWISS-PROT entry is copyright. It is produced through a collaboration
ខ	Decween the Swiss institute of bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
ည	as its content is in no
ဗ္ဗ ဗ္ဗ	modified and this statement is not removed. Usage by and for commercial putities requires a literal arranget (see bits. / frm. ish. cib. cib. ch. / commercial
ខ	or send an email to license@isb-sib.ch).
20 20	EMBI: MODODA AND TEAM O.
K K	
FT	
S0	DOMAIN 63 /0 POLY MET. SEQUENCE 403 AA; 39697 MW: 146FA642351D8E87 CRC64;
Öne	Ouery Match 19.0%; Score 111; DB 1; Length 403;
Mat	<pre>best Local Similarity 31.5%: Pred. No. 0.00071; Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps 7;</pre>
QY	-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIM
Ωp	118 GINTTESTINSPLDQALGINSTSQNDDSTSGTDSTSDSSDPMQQLLKMFSEIMQSLFGD 175
Qy	57 GSDANQECGNEQPONGQQEGLSPLTQMLMQIVWQLMQNQGGAGMGGGGSVNSSL 110

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "popA in Raistonia solanacearum OBI-1 pathogenic to tobacco.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Act as a specific hypersensitive response (HR) elicitor.
Has activity on tobacco (non-host plant) and petunia but is
without activity on tomato (host plant).
--- SUBCELLUIAR LOCATION: Secreted.
--- FUN: POPA2 and popA3 are produced from popA1 by stepwise removal of N-terminal amino acids.
Arlat M., Van Gijsegem F., Huet J.-C., Pernollet J.-C., Boucher C.A., "Pophl, a protein Which induces a hypersensitivity-like response on specific Petunia genotypes, is secreted via the Hrp pathway of Pseudomonas solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-GMI1000;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N
Gasplu C., Lavite M., Moisan A., Robert C., Saurin W., Schlex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                   PopAl protein [Contains: PopA2 protein; PopA3 protein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hikichi Y., Ikegami M., Okuno T.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypersensitive response; Plasmid; Complete proteome
                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                 POPA_RALSO STANDARD; PRT; 344 AA. 09RBSG; 022544; 09WXKC; 09RBYC; 03RAF2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-OE1-1;
Hikich Y., Kanda A., Hasegawa H., Okuno T.;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94148001; PubMed-8313899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB026629; BAA77270.1
AB032747; BAA84679.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 13:543-553(1994).
                                                                                                                                                                                                                                                                                                 Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-GMI1000;
                                                111 GGNA 114
                                                                               236 DGSS 239
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                                                                                                                                                                                                                                                                                                                                    Ralstonia
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                                                                                                                                                 POPA_RALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually rich in amino acid homopolymers."; Genes Dev. 4:1688-1700(1990).
                                                                                                                                                                                                                                                                                                                                                                         58 SAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQGPQSANKTGNVDDANNQDPMQALMQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                            118 LLEDLVKLLKAALHMOOPGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGG 177
                                                                                                                                                                                                                                                                                                            44; Gaps
                                                                                                                                                                                                                                                                                                                                       3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                           43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: MAY HAVE A REGULATORY FUNCTION POSSIBLY IN ASSOCIATION WITH THE N GENE PRODUCT.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- DEVELOPMENTAL STAGE: DURING EARLY NEUROGENESIS MAM PRODUCTS ARE UBIQUITOUSLY LOCATED. DURING LATER STAGES THEY ACCUMULATE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENTRAL NERVOUS SYSTEM.
MISCELLANEOUS: THE PROTEIN HAS MANY AA HOMOPOLYMERIC DOMAINS: 21
POLY-GLN RUNS (FROM 5 TO 16 AA IN LENGTH), 4 POLY-GLY (6 TO 10
AA), 3 POLY-ASN (3 X 5 AA), 1 POLY-ALA (10 AA) AND 1 POLY-THR (5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO OTHER NUCLEAR PROTEINS OF DROSOPHILA, TO CERTAIN YEAST AND MAMMALIAN REGULATORY PROTEINS.
                          POPAS PROTEIN.

POPAS PROTEIN.

TNS -> S (IN STRAIN OEI-1)

ANDESK -> GA (IN STRAIN 8107).

L -> P (IN STRAIN 8107).

G -> A (IN STRAIN 8107).

MISSING (IN STRAIN 8107).

ADG -> G (IN STRAIN OEI-1).

N -> I (IN STRAIN OEI-1).

G -> D (IN STRAIN OEI-1).

G -> D (IN STRAIN OEI-1).
                                                                                                                                                                                                                                                                         Length 344;
                                                                                                                                                                                                                                                                                                         55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CANTON-S;
MEDLINE-91065516; PubMed-1701150;
Smoller D., Friedel C., Schmid A., Bettler D., Lam L.,
Yedvobnick B.;
                                                                                                                                                                                                                       42A7C5A0C32B0907 CRC64
                                                                                                                                                                                                                                                                     18.8%; Score 110; DB 1; 25.8%; Pred. No. 0.00075; iive 16; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212
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                 PROTEIN.
 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurogenic protein mastermind.
                                                                                                                                                                                                                         Ψ.
                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                         40;
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P21519;
                                                                                                                                                                                     VARIANT
VARIANT
                                                                                                                                                                                                                       SEQUENCE
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the Euro
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                                                                                                                                                                                                                                                                                                         Matches
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FROM N.A.

Rieger

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and for commercial
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                    (See http://www.1sb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purnelle B., Skala J., van Dyck L., Goffeau A.; "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new TRNA gene and four new open reading frames including a leucine zipper protein and a homologue to the yeast mitochondrial regulator ABF2."; Yeast 10:125-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                QQHEDSSQQSPSAGSEQQLDQLLAMFIMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93342489; PubMed-8342024;
Brown S.J., Kellett P.J., Lippard S.J.;
"Ixrl, a yeast protein that binds to platinated DNA and confers
sensitivity to cisplatin.";
Science 261:603-605(1993).
                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Intrastrand crosslink recognition protein (Structure-specific
                                                                                                                                                                                                                                                                                                                                                                             16.5%; Score 96.5; DB 1; Length 1596; 28.8%; Pred. No. 0.087; Live 7; Mismatches 39; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTOQQITMQQQQQFVQSTTTTHQQQQMMQMGPGGGGGGGGGGGGSANNNGG 1525
                                                                                                                                                                                                                                                                     ALA-RICH.
8 X 2 AA TANDEM REPEATS OF V-G.
7 X 2 AA TANDEM REPEATS OF G-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...----QGGAGMGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                           AA TANDEM REPEATS OF G-V.
                                                                                                                                                                                                                                                                                                                           ASP/GLU-RICH (ACIDIC).
W; B944D86EF359D605 CRC64;
         ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
        Usage
                                                                                                                                   GLN-RICH.
ASN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 AA
modified and this statement is not removed entities requires a license agreement (See or Send an email to license@lsb-slb.ch).
                                                                                                                                                                              GLY/ASN-RICH
                                                                                                                                                                                        GLN-RICH.
GLY-RICH.
GLN-RICH.
                                                                                                             1; Repeat.
GLN-RICH.
                                                                                                                                                                                                                                            GLN-RICH.
5 X 2 AA
                                                                                                                                                                                                                                  GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recognition protein) (SSRP).
IXR1 OR ORD1 OR YKL032C OR YKL245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94262309; PubMed-8203146;
                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
                                                     EMBL; X54251; CAA38152.1; -.
                                                                                                                                                                                                                                                                                                                                       167717
                                                                   PIR, A33106, A33106.
PIR, A36391, A36391.
FlyBase, FBgn0002643; mam.
Neurogenesis; Nuclear prot
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                  1252
1496
1592
                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMIMOIVMOLMON----
                                                                                                                                                                                                                                                                                                                                         Ä.
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel
01-FEB-1995 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IXR1_YEAST
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                          DOMAIN
SEQUENCE
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                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IXR1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSDANQECG----NEQPQNGQQEGLSP----LTQMLMQIVMQLMQNQGGAGMGGGGSV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 QQQQQQQQQQQQQQQQQQQQQQVYYPLPPQSLTQPTSQSQQQQQQQQQQQQQANSNSNS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSIGNNFSNIG----NLQTMGI---GPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQ 56
                                                SEQUENCE FROM N.A.

MEDLINE-94316692; Pubmed-8041793;
Lambert J.R., Bilanchone V.W., Cumsky M.G.;
"The ORD1 gene encodes a transcription factor involved in oxygen regulation and is identical to IXRI, a gene that confers cisplatin sensitivity to Saccharomyces cerevisiae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00398; HMG; 2.
DNA-binding; Nuclear protein; Transcription regulation; Activator;
                                                                                                                                                      TO
                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 91:345-7349(1994).
-1- FUNCTION: BINDS TO PLATINATED DNA AND CONFERS SENSITIVITY
THE ANTICANCER DRUG CISPLATIN. ACTIVATE THE EXPRESSION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 597;
                        Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF3B705AA2C5AC74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Score 89.5; DB5; Pred. No. 0.15;14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y -> F (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> T (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOX 1.
BOX 2.
                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: CONTAINS 2 HMG BOXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA -> TT
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000910; HMG_12_box. Pfam; PF00505; HMG_box; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67856 MW;
                                                                                                                                                                                                                                                                                                                                        EMBL; X71622; CAB37853.1; -. EMBL; Z28032; CAA81867.1; -. EMBL; L16500; AAA02859.1; -. HSSP; P07155; 1AAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.3%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00398; HMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
207
220
220
297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            S0001515; IXR1
                                                                                                                                                                                                                                                                                                                                                                                                                FRANSFAC; T01849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 NSSLGGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNNVNVNA 134
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281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
93
                                                                                                                                                                              COX5B GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P300_HUMAN
ID P300_HUMAN
AC Q09472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
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Op
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2192 QQQQGAGPGIGPGMANHNQFQQPQGVGYPPQPQORMQHHMQQMQ-QG--NMGQIGQLPQA 2248
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          containing zinc fingers.";
Genetics 129:385-397(1991).
                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                      2249 LGAEA 2253
                                                    110 LGGNA 114
                                                                                                                                                                         BRC1_DROME
                                                                                                                                      RESULT 6
BRC1_DROME
                                                                                      q
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                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                              MEDLINE-95011587; PubMed=7523245; Eckner R., Even M. E., Newsome D., Gerdes M., Decaprio J.A., Eckner R., Livingston D.M.; Eckner C. July Strong D.M.; Livingston D.M.; Molecular cloning and functional analysis of the adenovirus Elassociated 300-kD protein (p300) reveals a protein with properties of at transcriptional adaptor. ; Genes Dev. 8:869-884(1994). ; FUNCTION: PROBABLE TRANSCRIPTIONAL ADAPTOR REQUIRED FOR THE ACTIVITY OF CERTAIN COMPLEX TRANSCRIPTIONAL REQUIRED FOR THE MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS ELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2132 NMNPMQAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQMNMNHNTMPSQFRDILRRQQMMQQ 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 QOSQGSDANQECG---NEQPQNGQQEGLSPLTQMLMQIVMQLMQNQGGAGMGGGGGSVNSS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 NLQTMGIG-----PQQHEDSSQQSPSAGSEQQLDQ------LLAMFIMMML 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50135; ZF_ZZ_2; 1.
Transcription regulation; Nuclear protein; Bromodomain; Cell cycle;
Zinc-finger.
                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING REGION FOR E1A ADENOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 88; DB 1; Length 2414;
Pred. No. 0.96;
5; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6BFF909EE4B9D693 CRC64;
                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
01-MAR-2002 (Rel. 41, Last annotation update)
ElA-associated protein p300.
EP300 OR P300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER.
POLY-GLU.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PRODSO3; BROMODOMAIN.
SMART; SMO0297; BROMO; 1
BRORTIE; SMO0291; ZNF_ZZ,
PROSITE; PSO0014; BROMODOMAIN_1;
PROSITE; PSSO014; BROMODOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001487; Bromodomain.
InterPro; IPR003101; KIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000197; TAZ_finger.
InterPro; IPR000433; ZnF_2Z.
Pfam; PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                              Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U01877; AAA18639.1; -
TRANSFAC; T01427; -.
MIM; 602700; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%;
31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       '; ZF_ZZ_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264143
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Pfam; PF02135; zf-TAZ; 2.
Pfam; PF00569; ZZ; 1.
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1139
1818
1707
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2069
2195
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                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 39; Conserv
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Query Match

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SEQUENCE

DOMAIN ZN_FING DOMAIN DOMAIN

DOMAIN DOMAIN OMAIN DOMAIN

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RAINTH-EBREALLEY;
RAY MEDLINE-20196006; PubMed-10731132;
RAINTH-EBREALLEY;
RA Amanatides P. G. Scherer S. E., Holf R. R., Hoskins R. A., Galle R.F.,
RA Amanatides P. G. Scherer S. E., Li P. W., Hoskins R. A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburnar M., Henderson S.N.,
RA Sutton G.G., Wortman J. R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RADII J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Blottler P.,
RADII J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Blottler P.,
RADII J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cavley S., Dallke C., Davenport L.B., Davies P.,
RADORON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RADORON K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RADORON K., Gabriellan A.E., Garry N.S., Gelbart W.M., Glasser R.,
RADORON K., Gabriellan A.E., Garry N.S., Gelbart W.M., Glasser R.,
RADORON K., Gabriellan A.E., Garry N.S., Gelbart W.M., Glasser R.,
RADORON K., Gong F., Gorriell J.H., Gu Z., Guan P., Harris M.,
RADIAI M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
Allain M., Kalush F., Kalpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RAMINGL B.E., Kodira C.D., Kraft C., McLeod M.P., McThy W. Murphy B., Murphy L., Murny D.M., Nelson D.L.,
Radon D.R., Woyler W., Murphy B., Murphy L., Murny D.M., Nelson D.K.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
Spiers E., Spradling A.C., Stapleton M., Skupeki M.P., Smith R.,
Spier E., Spradling A.C., Zaveri J.S., Zhun X., Zhu S., Zhu S
                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DiBello P.R., Withers D.A., Bayer C.A., Fristrom J.W., Guild G.M.; "The Drosophila Broad-Complex encodes a family of related proteins
                                  Q01295; Q01296; Q01293; O46066; Q9W574; O46065; Q9W571; O1-NOV-1995 (Rel. 32, Created)  
16-OCT-2001 (Rel. 40, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
Broad-complex core-protein isoforms 21/22/23 (BRCORE).  
BR OR BR-C OR EG:17A9.1 OR EG:25D2.1 OR EG:123F11.1 OR CG11491 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., CHARACTERIZATION, AND ALTERNATIVE SPLICING. STRAIN-OREGON-R; TISSUE-Larva; MEDLINE-92077389; Pubmed-1743483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS INT1-Q1-Z1 AND NS-Z3).
727 AA
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Bayer C.A., Holley B., Fristrom J.W.
"A switch in broad-complex zinc-finger isoform expression is regulated posttranscriptionally during the metamorphosis of Drosophila imaginal
                                             Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden Kiamos I., Bolshakov S.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaeftler P., Werner M., Mourkioti F.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
MCMIllan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
                                                                                                                                                                                                                                                                                                                                                                     "Puffs and PCR: the in vivo dynamics of early gene expression during ecdysone responses in Drosophila.";
Development 118:613-627(1993).
                                                                                                                                                                       From sequence to chromosome: the tip of the X chromosome of D.
            EQUENCE FROM N.A. (ISOFORMS TNT1-Q1-Z1; Z2 AND NS-Z3).
                                                                                                                                                                                                                     DEVELOPMENTAL STAGE, AND CHARACTERIZATION OF ISOFORMS.
                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF ISOFORMS, AND MUTATIONAL ANALYSIS
                                    MEDLINE-20196011; PubMed-10731137;
                                                                                                                                                                                                                                 TISSUE-Larva, and Imaginal disks;
MEDLINE-96299417; PubMed-8660872;
                                                                                                                                                                                                                                                                                                                                               MEDLINE-94038699; PubMed-8223281;
Huet F., Ruiz C., Richards G.;
                                                                                                                                                                                             Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                           Dev. Biol. 177:1-14(1996)
                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE.
                                                                                                                                                                                    melanogaster.
                                                                                                                                                             Glover D.M.;
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RY MEDLINE-97384928; PubMed-92423;

RA BADELTON OF ISOPORNS, AND MUTATIONAL ANALYSIS.

BAYET C.A., von Kalm L., Fristrom J.W.;

BADELTOSHIPS between protein isoforms and genetic functions demonstrate functional redundancy at the Broad-Complex during Drosophila metamorphosis.";

Drosophila metamorphosis.";

Drosophila metamorphosis.";

1- FUNCTION: BROAD-202(1997).

1- FUNCTION: BROAD-202(1997).

1- FUNCTION: BROAD-202(1997).

1- SUBCELLUAR LOCATION: NUCLEAR.

1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; BRCORE-TWIT-01-21 (SHOWN HERE); BROORE-02-22, BROCHE-NS-23 AND BRCORE-24.

1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; BRCORE-TWIT-01-21 (SHOWN HERE); BROORE-02-21, BROCHE-NS-23 AND BRCORE-24.

1- ALTERNATIVE PRODUCTS: 6 ISOFORMS; BRCORE-TWIT-01-1 (SHOWN HERE); BROORE-02-11, BROORE-22, BRCORE-NS-23 AND BRCORE-24.

1- ALTERNATIVE ALLOPANT AT BECINNING OF ECUPSONE RESPONSE (94-114 HOURS OF DEVELOPMENT IN LATE ENGINING OF ECUPSONE RESPONSE (94-114 HOURS OF DEVELOPMENT IN LATE ENGANGES 3-10. IN REPURPER STAGE 15 ONWARDS, REACHING MAXIMUM AT THE MADEL AND BECOME THE PREDOMINANT IN LEVELS REMAIN CONSTANT BETWEEN STAGE 1-11 AND HOURSACE 1-11 AND HOURS AT STAGE 15 ONWARDS, REACHING MAXIMUM AND STAGES 18-20. IN GUT, LEVELS REMAIN CONSTANT BETWEEN STAGE 1-11 AND ABROUPLY DISAPPEARS AT BODY AND WING DISKS, LOW LEVELS IN REPURPER STAGE 1-1 AND ABROUPLY DISAPPEARS AT BODY AND WING DISKS, LOW LEVELS IN A HUR LEVELS IN A HUR LATE BECTNNING OF THE ECDYSONE RESPONSE DURING OF THE ECDYSONE PREVENCE ARE SEEN IN THE MING DISK. ISOFONA 23; IN MID INSTAAR LARVAL SALIVARY GLAND THEN HUR DISK TAGE 11. IN PREPURPES STAGES 11. AND ABROUPLY DISAPPEARS ATTER SEVERAL HOURS. LEVELS AT HERE BECONSONE, 94-99 HOURS OF DEVELOPMENT IN PUFF STAGE 11. AND ABROUPLY DISAPPEARS ATTER SEVERAL HOURS. LEVELS AT HERE SEVERAL HOURS. LEVELS AT HERE SEVERAL HOURS. LEVELS BY DIFF STAGE 11. IN MAING DISK. LEVELS AT HOURS. TRANSCRIPTS ARE BENDINGHAD AND THE BECONSONE, 94-99 HOURS O LOW LEVELS IN WING DISK.
INDUCTION: PRIMARY RESPONSE TO 20-HYDROXYECDYSONE IN THIRD INSTAR

ò q SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN. LARVAL IMAGINAL DISKS.

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P20393
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ZN_FING
ZN_FING
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                                                                                                                    Aedes
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                                                                                                                                                          Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                         MEDLINE-91246165; PubMed-1903840; Yao K.-M., White K.; Organizational analysis of elav gene and functional analysis of ELAV protein of Drosophila melanogaster and Drosophila virilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 LQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQ 73
                                                                                                                                                                                                                                                                                    MOI. Cell. Biol. 11:2994-3000(1991).
-!- FUNCTION: PROBABLY INVOLVED IN THE RNA METABOLISM OF NEURONS.
-!- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
-!- SIMILARITY: BELONGS TO THE ELAV FAMILY OF RNP PROTEINS.
65 GNEQPONGQOEGLSPL----TQMLMQIVMQLMQNQGGAGMGGGGGSVNSSLGGN 113
                Query Match

14.8%; Score 86.5; DB 1; Length.519;
Best Local Similarity 27.8%; Pred. No. 0.25;
Matches 27; Conservative 14; Mismatches 49; Indels
                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elav protein (Embryonic lethal abnormal visual protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOLAFICODEOIBOD9 CRC64;
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RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 QEGLSPLTQMLMQIVMQLMQ--NQGGAGMGGGGSVNS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 QQQQQVVQQQVQQQANTNGNSGGAQNGSNGSTET 183
                                                                                519 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALA/GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A40252; A40252.
HSSP; P19339; 2SXL.
TyBase; FBgn0013110; Dvir\elav.
InterPro; IPR002343; Hud_Sxl_RNA.
InterPro; IPR000504; RRM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55822 MW;
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PROSITE; PS00030; RRM_RNP_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M61748; AAA28505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00076; rrm; 3.
PRINTS; PR00961; HUDSXLRNA.
SWART; SM00360; RRM; 3.
                                                                               STANDARD;
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                                                                              ELAV_DROVI
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                                                                                                                        Aedes aegypti (Yellowfever mosquito).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE: PS00031; MUCLEAR. RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. NRI SUBFAMILY.
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HORMONE-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129B6EA8A76F4918 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODULATING (POTENTIAL)
NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001023; Strdhormone_receptor.
InterPro; IPR001023; Strdhormone_receptor.
Pfam; PF00104; hormone_rec; 1.
Pfam; PP00105; zfrc4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
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                                                                                                                                                                                                                                                                             TISSUE=Fat body;
MEDLINE=95227190; PubMed=7711747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MM;
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29.68;
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                                                                              receptor) (20E receptor).
ECR OR NR1H1.
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616
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Best Local Similarity
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.G., Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Gutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R.A. Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,
R.A. Abril J.F., Agbayaid A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
R.A. Abril J.F., Basendale J., Bayraktaroglu L., Beasley E.M.,
R.A. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R.A. Bernos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Borkova D., Botchan M.R., Buuck J., Brokstein P., Brottier P.,
R.A. Cherry J.M., Cawley S., Dahlker H., Cadieu E., Center A., Chandra I.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R.,
R.A. Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Ketchum K.A.,
R.A. Harris N.L., Harvey D., Heinan T.J., Wei M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R.M. Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
Lian Y., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
R. McMarle B.C., Kratter C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                  12.2. no. 0. 17. Created)
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 07, Last montation update)
16-OCT-2001 (Rel. 07, Last montation update)
17-EB-08 (Rel. 07, Last montation update)
18-OR FPILD ON BYELD (TATA-box factor) (TATA-sequence-binding protein) (TBP) (TATA-box binding protein).
18-OR FPILD ON BYEL OR CG984.
18-OR FPILD ON BYEL OR CG984
                                                        22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMILQQSQG-SDANQECGNEQPQNGQQ----E 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90304877; PubMed-2194666;
Hoey T., Dynlacht B.D., Peterson M.G., Pugh B.F., Tjian R.;
"Isolation and characterization of the Drosophila gene encoding the
TATA box binding protein, TFIID.";
Cell 61:1179-1186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muhlch M., Iida C.T., Horikoshi M., Roeder R.G., Parker C.S., "cDNA clone encoding Drosophila transcription factor TFIID."; Proc. Natl. Acad. Sci. U.S.A. 87:9148-9152(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee R., Oh Y., Yoon J., Cho N., Baek K.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lira-Devito L.M., Burke T.W., Kadonaga J.T.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                        627 QLTPNQQQHQQQHSQLQQVHANGSGGGGSNNNSSGG 664
                                                                                                                                                                                                                                                                                                                                                               353 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91067664; PubMed=2123550;
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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TF2D_DROME
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nisskern D.R., Pacleb J.M.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Santh T.,

Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Ry Spier E., Spradling A.C., Stapleton M., Weissenbach J., Mang X.,

Ry Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

Milliams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

Milliams S.M., Myers E.W., Rubin G.M., Venter J.C.;

Ry Chorn Sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000)

C. - FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION

OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS

SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO

C. - C. TENDERM. THE POSITION OF TRANSCRIPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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POLY-GLN.
POLY-GLN.
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Pred. No. 0.36; . .
9; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> A (IN REF. 4).
7B079BC01BAF69BC CRC64;
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                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: BINDS DNA AS A MONOMER.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE TBP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1480 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 TQMLMQIVMQLMQNQ--GGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 TPQSMMAHMMPMSERSVGGSGGGGGDALSNI 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M38082; AAA28931.1; --
EMBL; U1718; AAA68629.1; --
EMBL; U35147; AAA79092.1; --
EMBL; AE003454; AA46754.1; --
PIR; A35615; A35615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation;
DOMAIN 54 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIYBase; FBgn0003687; Tbp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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353 AA;
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TRANSFAC; T00797
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P32521;
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PAN1_YEAST
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NCBI_TaxID-4565;
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P08488;
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                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: NOT KNOWN.
-!- PTW: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: SOME TO MAMMALLIAN EPS15.
-!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A SUBUNIT OF PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE.
                                                                                                                                                                                                                                                                                          Voss H., Tamames J., Teodoru C., Valencia A., Sensen C., Wiemann S., Schwager C., Zimmermann J., Sander C., Ansorge W.; "Nucleotide sequence and analysis of the centromeric region of yeast chromosome IX.";
                                                                                                                                                                  STRAIN S288C / AB972;
Barrell B.G. Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear.S., Deviln K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream W.A., Riles L., Rowley N., Skelton J., Smith V., Whitehead S., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                   Saccharomycetes;
                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 320-344; 352-375 AND 899-906. MEDLINE-92405166; PubMed=1339314; Sachs A.B., Deardorff J.A.; "Translation initiation requires the PAB-dependent poly(A) ribonuclease in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA APPROXIMATE REPEATS
                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ašcomycota; Saccharomycotina;
  Last sequence update)
                             OR MIP3 OR MDP3 OR YIR006C OR YIB6C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 x 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; $30889; $30889.
IF; $44440; $48440.
SGD; $0001445; PAN1.
InterPro, IPR000261; EPS15_repeat.
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1-3.
1-3.
1-5.
1-6.
1-7.
1-9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z38062; CAA86208.1; -. EMBL; M90688; AAA34841.1; -. EMBL; X79743; CAB38097.1; -.
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403
420
433
509
518
549
01-FEB-1995 (Rel. 31, 01-NOV-1997 (Rel. 35,
                                                                                                                                        Cell 70:961-973(1992)
                                                                                                                                                                                                                                                                                                                                (east 11:61-78(1995)
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                           SEQUENCE FROM N.A
                                                                     NCBI_TaxID-4932;
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DOMAIN
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GGVLPPPPPLPQQASTSEP1IAHVDNYNGAEKGTGAYGS
DSDDDVLSIPESVGTDEEEEGAQPVSTAGIPSIPPAGIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPPLP -> EAFCLHPHLYQLNKLPLQNLLSLTLITTMVL
KKARAHMDPILMMTFYRFLNQLVQMKRKKGHNQFLLQVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. CHINESE SPRING;
MEDLINE-86041802; PubMed-31840588;
Thompson R.D., Bartels D., Harberd N.P.;
"Nucleotide sequence of a gene from chromosome 1D of wheat encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 QTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQ---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QQQCMGYQQQQQQQQQQPNG-----FYPQQQQGQSSNQPQGQPQPQQMA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                        P -> T (IN REF. 1).
ITAQDQAK -> YYCPRSGKN (IN REF. 1).
MISSING (IN REF. 1).
MISSING (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFHLQVFLHPHPFHEDLICFL (IN REF. 1)
W; F3518495FF759553 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82.5; DB 1; Length 1480;
Pred. No. 2;
9; Mismatches 44; Indels 23
              1-15.
2 x 23 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 --NGQQEGLSPLTQMLMQIVWQLMQNQGGAGMGGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit 12 precursor.
                                                                           AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 FNQPQATGIGGMPQSFGNSFSSMPQ-OPQTGYNNGN-NGSVYGN
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POLY-PRO.
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2-2.
7 x (
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3 x
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Best Local Similarity 27.6%;
Matches 29; Conservative
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556
575
680
350
680
1125
1089
1095
1101
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1125
1377
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1345
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1360
1366
1377
22
34
106
1406
1480
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416 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLTO_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLU-D1-2B.
                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheyenne.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                  -i-MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP 1 CHROMOSOMES OF WHEAT.
-i-MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQQPGQ AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 GOWQOSGOGOGHYPTSLQOPGOGOO----GHYLASQOQPAQGOGGHYPASQQOPGQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van der Spek P.J., Visser C.E., Hanaoka F., Smit B.,
Hagemeijer A., Bootsma D., Hoeijmakers J.H.J.;
"Cloning, comparative mapping, and RNA expression of the mouse
homologues of the Saccharomyces cerevisiae nucleotide excision repair
gene RAD23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 31:20-27(1996).
-!- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
                                                                                                                                                                                                                                                                                                                                          GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 GNLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQN 71
                            STORAGE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
UV exclsion repair protein RAD23 homolog B (MHR23B) (XP-C repair complementing complex 58 kDa protein) (P58).
                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                             13.9%; Score 81; DB 1; Length 660; 27.4%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 GOOEGLSPLTQMLMQIVMQLMQNQGG-----AGMGGGGSVNSS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 GQQ-GHYPASQ-----QQPGQGQQGHYPASQQEPGQQQQQIPAS 355
                                                                                                                                                                                                                                                                                                                 Seed storage protein; Repeat; Multigene family; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            2BFD09D8C8FCCCFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
                                                                                                                                                                                                                                                               InterPro: IPR001768; Cereal_tryp_amyl_inh.
InterPro: IPR001419; Glutenin.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                 REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C; TISSUE-Testis;
MEDLINE=96403997; PubMed=8808275;
                                                                                                                                                                                                                                                                                                                                                                           70868 MW;
                                                                                                                                                                                                                               EMBL; X03041; CAA26847.1; -. PIR; A24266; A24266.
HSSP; P01088; 1BFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                 GOOPGOGOGGYPTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                               125 6
660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAD23B OR MHŘ23B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R23B_MOUSE
P54728;
                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R23B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
q
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 QQMRQIIQQNPSL-----LPALL-------QIGRENPQLLQQ--ISQHQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Malpica-Romero J.M.; "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 17:461-462(1989).
-1- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum (Wheat).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta.
CHROMATIN STRUCTURE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.,
                        ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.
SUBUNIT: HETERODIMER OF A 125 kDa SUBUNIT (P125) AND OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit DY10 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13E0245A6D892205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                      58 kDa SUBUNIT (P58).
-1- SUBCELLGLAR LOCATION: Nuclear (Probable).
-1- SIMILARITY: CONTAINS 1 UBLQUITIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 2 UBA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 79; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UBIQUITIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       648 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.1;
9; Mismatches
   RECOGNITION AND/OR IN ALTERING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QMLMQIVMQLMQNQGGAGMGGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA damage; DNA repair; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-ALA.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50053; UBIQUITIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. CHEYENNE;
MEDLINE=89098419; Pubmed=2563152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:105128; Rad23b.
InterPro; IPR0000449; UBA.
InterPro; IPR0000526; Ubiquitin.
Pfam; PF00627; UBA; 2.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X92411; CAA63146.1; -. HSSP; P54725; 1DV0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00165; UBA; 2.
SMART; SM00213; UBQ; 1.
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HSSP; P09651; 1HA1
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LP61_EIMTE
P15714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZN_FING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
           SOURCE STATE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéfisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-!- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES. ...
-!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 SLOOPGOGOOGHYLASQOOPGOGOO-----GHYPASQOOPGOGOOGHYPASQOOPGOG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 NLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alliegro M.C.;
"A C-terminal carbohydrate-binding domain in the endothelial cell
regulatory protein, pigpen: new function for an EWS family member.";
Exp. Cell Res. 255:270-277(2000).
                                                            GROUP I CHROMOSOMES OF WHEAT.
MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GOOPGO AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alliegro M.C., Alliegro M.A.;
An unclear protein regulated during the transition from active to
quiescent phenotype in cultured endothelial cells.";
Dev. Biol. 174:288-297(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%; Score 79; DB 1; Length 648; 29.8%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seed storage protein; Repeat; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEATS.
FE98F1D44B9E9AF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
RNA-binding protein FUS (Pigpen protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 QOEGLSPLTOML ---- MQIVMQLMQNQGGAGMGG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 00-GHYPASQQEPGGGQGGIPASQQQPGQGQQG 353
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001419; Glutenin.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20160719; PubMed-10694442; Alliegro M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Aorta;
MEDLINE-96175600; PubMed-8631501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69629 MW;
                                                                                                                                                                                                                                                                                                                                                EMBL; X12929; CAA31396.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYDRATE BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.5°
Best Local Similarity 29.8°
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                      PIR; S04832; S04832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 taurus (Bovine).
                                                                                                                                 GOOPGOGGGYPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUS_BOVIN
Q28009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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FUS_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-STRANDED DNAS. AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED DNA. MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY (BY SIMILARITY).
                                                                                                                                                                                                         THROUGHOUT (EXCLUDING NUCLECAL), TOGETHER WITH A SMALL NUMBER OF INTENSELY STAINED FOCAL POINTS, OR GRANULES, AND PUNCTATE STAINING ALONG THE NUCLEAR ENVELORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS5010; RRM; I. FALSE_NEG.
PROSITE; PS501030; RRM_RNP_1; FALSE_NEG.
PROSITE; PS50199; ZF_RANBP2_1; 1.
PROSITE; PS50199; ZF_RANBP2_2; 1.
Mexal-binding; DNA-binding; Nuclear protein; Repeat; Zinc-finger; Zinc; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 QSSGYGQPQGGGYGQQSGYGGQQQSYGQQQSYNPPQGYGQQSQYNSSGGGGGGGGGGSYGQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 QTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMML-QQSQ-----GSDANQECGN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 EQPQ------NGQQEGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR, EXHIBITS DIFFUSE STAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 512;
                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE C-TERMINAL DOMAIN BINDS CARBOHYDRATES.
SIMILARITY: CONTAINS I RNA RECCONITION MOTIF (RRM).
SIMILARITY: CONTAINS I RANBP2-TYPE ZINC FINGER.
SIMILARITY: BELONGS TO THE TET FAMILY OF NNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78.5; DB 1; Length 51
Pred. No. 1.5;
6; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3652329C044F1386 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLN/GLY/SER/TYR-RICH.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-BINDING (RRM).
ARG/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANBP2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000504; RRM.
InterPro; IPR001876; Znf-RanBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52240 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U26024; AAC13543.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%;
29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00360; RRM; 1.
SMART; SM00547; ZNF_RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen LPMC-61 (Fragment).
Elmeria tenella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
253
357
512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357
408
512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                  SUBUNIT: MAY BE COVALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO FORM THE 80 kDa ANTIGEN.
DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE SPORULATION OF THE OCCYSTS AND IN THE SPOROZOITES FOLLOWING
                                                                                                                                                                                                                                                                                                 12 X APPROXIMATE TANDEM REPEATS, GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8C5E6005FFFC2DB3 CRC64;
                                                                                                                                                                                                                                                   Antigen: Sporozoite; Repeat; Sporulation.

NON_TER 1

DOWAIN 18
            90348718; PubMed-2200963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      255
31267 MW;
                                                                                     IMPORTANT IMMUNGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    255
255 AA;
                                                                                                                                          EXCYSTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
NON_TER
SEQUENCE
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                           EPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                EPEAT
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Gaps ... Score 78; DB 1; Length 255; Pred. No. 0.79; 6; Mismatches 48; Indels Query Match 13.4%; Best Local Similarity 32.6%; Matches 30; Conservative å

5

22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81

g

82 QMLMQIVMQLMQNQGGAGMGGGGSVNSSLGGN 113 ò

198 OOPOO--OOQOOOOOOLGPDGVGIVVPYLGSS 227

g

Search completed: June 28, 2002, 10:22:46 Job time: 168 sec